

FT	Domain	240..260
FT		/note="Transmembrane domain"
XX		
PN	WO200139722-A2.	
XX		
PD	07-JUN-2001.	
XX		
PE	30-NOV-2000; 2000WO-US32583.	
XX		
PR	30-NOV-1999; 99US-0451291.	
PR	28-AUG-2000; 2000US-0649108.	
XX		
PA	(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.	
XX		
PI	Chen L;	
XX		
DR	WPI; 2001-397926/42.	
DR	N-PSDB; AAS06592.	
XX		

Novel DNA encoding immunoregulatory molecule B7-H1, is useful for co-stimulating a T cell for augmenting immunoregulation and for controlling pathologic cell mediated conditions -

Claim 9; Fig 2A; 85pp; English.

CC The present sequence representing novel human immunoregulatory protein
CC B7-H1 (hB7-H1) is capable of co-stimulating T-cells. The sequence for
CC mouse B7-H1 (mB7-H1) is also given (AAU03560). B7-H1 is useful for
CC co-stimulating T-cells such as helper T-cells that provide helper
CC activity for B-cell antibody-producing response e.g. 19G2a antibody
CC response, in a mammal having an immunodeficiency disease, inflammatory
CC condition or an autoimmune disease. By culturing B7-H1 with the
CC mammalian T-cells in vitro, or administering B7-H1 or a nucleic acid
CC encoding B7-H1 to the T-cells, such that the level of CD40 ligand on the
CC T-cell surface is increased. The method further involves providing a
CC recombinant cell e.g. an antigen presenting cell (APC) which is the
CC progeny of a cell obtained from the mammal and has been transfected or
CC transformed *ex vivo* with a nucleic acid encoding B7-H1, so that the cell
CC expresses B7-H1, and administering the cell to the mammal. Prior to
CC administration, the APC is pulsed with an antigen or an antigenic
CC peptide. B7-H1 can be used to control pathologic cell mediated
CC conditions (e.g. those induced by infectious agents such as Mycobacterium
CC tuberculosis) or other pathologic cell mediated responses such as those
CC involved in autoimmune diseases (e.g. rheumatoid arthritis).

	Query Match	100.0%	Score 1511	DB 22	Length 290
	Best Local Similarity	100.0%	Pred: No. 7.3e-135		
	Matches 290	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 KRIFVFIFMTYMWHLNMFVTVPKPDLYVVEGSMNTECKRPVEKQDLALIVYWE				60
Db	1 mrltavlflfmylwnlhnltvcpdxllyveygsmtleackfprveqjdaaalivyme				60
QY	61 DKNIQFHGEEDLVVOHSSYRQARRLKDLQSLGNALQIIDVVKIQDAGYRCMTSYG				120
Db	61 dknliqfghgeedlkvghssyqrarllkdqslslnaalqldcvklqdagvgrycmisyyg				120
QY	121 ADYKRITVKVNAPYKINQRIILVDPVTSSEHLETCOAEQYPAEVLWTSDDHQVLSGKTT				180
Db	121 adykriltvkvnaryklingrlilvdpvtsesehelctgaeyrkaevlwtssdhqvlsgktt				180
QY	181 TTNSKREKELFNWSTLKRLNTTNEILFICTFPRRLDPEENHNLVLPILPLAHPNERH				240
Db	181 ttnskreeklfnvstclrlnttneilfictfprrldeeenhnlvlpilplahpnerh				240
QY	241 LVITGAILLGCVALTFTFRLLKGMNMDVKKGIQDTNSKKSDPHLEET				290
Db	241 lvitgaillcgvalltftfrllkgsmdvdkcgldttnskksdphleet				290

RESULT	2
AAE01164	
ID	AAE01164 standard; Protein; 290 AA.
XX	
AC	
XX	AAE01164:
DT	17-JUL-2001 (first entry)
XX	
DE	Human gene 1 encoded secreted protein B7-H6, SEQ ID NO:65.
XX	
KW	Human; secreted protein; proliferative disorder; cancer; tumour;
KW	fetal abnormality; developmental abnormality; haematological disorder;
KW	immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW	Inflammation; allergy; neurological disorder; Alzheimer's disease;
KW	Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW	skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW	cardiovascular disorder; angiodysplasia; kidney disorder;
KW	gastrointestinal disorder; pregnancy-related disorder; B7-H6 protein;
KW	endocrine disorder; infection; wound healing; vulnerability; gene therapy;
KW	cell culture; chemotaxis; food additive; chromosome 9;
KX	
RN	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..18
FT	/label= Signal_peptide
FT	Protein
FT	19..290
FT	/label= Mature_human_B7_H6_secreted_protein
XX	
RN	WO200134768-A2.
PD	
PD	17-MAY-2001.
XX	
XX	01-NOV-2000; 2000MO-US30039.
PF	
XX	
PR	09-NOV-1999; 99US-0164344.
PR	07-APR-2000; 2000US-0195296.
PR	27-JUL-2000; 2000US-0221367.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	
OL	Olsen HS, Komatsu G, Duan DR, Ebner R, Ruben SM,
DR	WPI: 2001-308780/32.
N	N-PSDB: AAD05053.
PT	Isolated nucleic acid molecule encoding a human secreted protein is
XX	used in preventing, treating or ameliorating a medical condition -
XX	
XX	Claim 11; Fig 1; 474pp; English.
XX	
CC	AAD05053-AA05106 represent cDNAs corresponding to 15 human secreted
CC	protein genes, and AAE01164-AAE01217 represent the proteins they encode.
CC	AAE01218-AAE01226 represent human secreted protein fragments or variants
CC	The secreted proteins and their genes are useful for preventing,
CC	treating or ameliorating medical conditions, e.g., by protein or gene
CC	therapy. Pathological conditions can be diagnosed by determining the
CC	amount of the new protein in a sample or by determining the presence of
CC	mutations in the new genes. Specific uses are described for each of the
CC	15 genes, based on the tissues in which they are most highly expressed,
CC	and include developing products for the diagnosis or treatment of
CC	proliferative disorders, cancer, tumours, fetal and developmental
CC	abnormalities, hematopoietic disorders, diseases of the immune system,
CC	AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC	allergies, neurological disorders (e.g., Alzheimer's disease,
CC	Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC	skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC	cardiovascular disorders, angiodysplasia, kidney disorders,
CC	gastrointestinal disorders, pregnancy-related disorders, endocrine
CC	disorders, and infections. The proteins can also be used to aid wound
CC	healing and epithelial cell proliferation, to prevent skin aging due to
CC	sunburn, to maintain organs before transplantation, for supporting cell

Query Match	100.0%	Score 1511	DB 22	Length 290
Best Local Similarity	100.0%	Pred. No. 7.3e-135		
Matches 290	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	1	MRIFVFIFPMYWHILNFTVTPRKDLVYVEGSMWTIECKRPVEKQDLALIVYWE	60	
Db	1	mltavlflfmywhlnhnlavltvprdllyvegsnmileckrpvekqdlalivyme	60	
61	DKNIIQFHEGDEDLKVQHSYRQARARLLKDLQSLGNALQITDYLQDAGVYRCMTISYG	120		
Db	61	dknllqfthgeedlkvqhsyrgqrarllkdqslsgnaalqitdvlqdaqyvrchlsyrg	120	
OY	121	ADYKRITVKNAPYKINORILLVDPVTSSEHETLQCAEGYRKAEYIWTSSDHVLSGKTT	180	
Db	121	adykriltvknapyklnqrillvdpvtssehelctqeaqyrkaevlwtssdhvlsqkt	180	
OY	181	TTNSRKREELKPNVSTLRINTTNEIFCTPRRLDPRENNHRAELVIPLELPAHPNERTH	240	
Db	181	tnnsrkeelknvstlrinttneifctprrldprennhraelviplelphhpnerth	240	
OY	241	LVILGAILLCGLVALTFTRLLKRGHMDVKKCGIDOTNSKKOSDPHLEET	290	
Db	241	lvilgailclgvaltftrllrkghmdvkkcgidotskksdpdhleec	290	
RESULT 3				
ID	AAU01362			
XX	AAU01362 standard; Protein: 290 AA.			
AC	AAU01362;			
XX				
DT	18-JUL-2001 (first entry)			
XX				
DE	Human TANGO 509 amino acid sequence.			
XX				
KY	Human; TANGO 509; transmembrane protein; diagnostic; asthma; immunological disorder; arthritis; graft rejection; renal disorder; acquired immunodeficiency syndrome; inflammatory disorders; psoriasis; AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pituitary; Cushing's disease; neurodegenerative disease; Parkinson's disease.			
KW				
XX				
OS	Homo sapiens.			
XX				
FT	Key	Location/Qualifiers		
FT	Peptide	1..18		
FT	Protein	/note= "Signal peptide"		
FT	Domain	/note= "Mature TANGO 509"		
FT	Domain	19..240		
FT	Domain	/note= "Cytoplasmic domain"		
FT	Modified-site	33..113		
FT	Modified-site	/note= "Immunoglobulin (Ig)-like domain"		
FT	Modified-site	33..38		
FT	Modified-site	/note= "N-myristylation site"		
FT	Modified-site	35..38		
FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	Modified-site	80..82		
FT	Modified-site	/note= "Protein kinase C phosphorylation site"		
FT	Modified-site	105..112		
FT	Modified-site	/note= "Tyrosine kinase phosphorylation site"		

FT	Modified-site	110..115	
FT	/note= "N-myristylation site"		
FT	Modified-site	124..127	
FT	/note= "cAMP- and cGMP-dependent protei kinase phosphorylation site"		
FT	Modified-site	127..129	
FT	/note= "Protein kinase C phosphorylation site"		
FT	Modified-site	149..152	
FT	/note= "Casein kinase II phosphorylation site"		
FT	Modified-site	168..171	
FT	/note= "Casein kinase II phosphorylation site"		
FT	Modified-site	176..178	
FT	/note= "Protein kinase C phosphorylation site"		
FT	Modified-site	184..186	
FT	/note= "Protein kinase C phosphorylation site"		
FT	Modified-site	184..187	
FT	/note= "Casein kinase II phosphorylation site"		
FT	Modified-site	192..195	
FT	/note= "Asn is N-glycosylated"		
FT	Modified-site	196..198	
FT	/note= "Protein kinase C phosphorylation site"		
FT	Modified-site	200..203	
FT	/note= "Asn is N-glycosylated"		
FT	Modified-site	202..205	
FT	/note= "Casein kinase II phosphorylation site"		
FT	Modified-site	210..212	
FT	/note= "Protein kinase C phosphorylation site"		
FT	Modified-site	219..222	
FT	/note= "Asn is N-glycosylated"		
FT	Domain	241..259	
FT	/note= "Transmembrane domain"		
FT	Modified-site	252..257	
FT	/note= "N-myristylation site"		
FT	Domain	260..290	
FT	/note= "Extracellular domain"		
FT	Modified-site	273..278	
FT	/note= "N-myristylation site"		
FT	Modified-site	279..281	
FT	/note= "Protein kinase C phosphorylation site"		
FT	Modified-site	285..288	
FT	/note= "Casein kinase II phosphorylation site"		
XX			
XX	WO200121631-A2.		
XX			
XX	29-MAR-2001.		
XX			
XX	20-SEP-2000; 2000WO-US25982.		
XX			
XX	20-SEP-1999; 99US-0399723.		
XX			
XX	(MILL-) MILLENNIUM PHARM INC.		
PA			
PI	Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury C.		
XX			
XX	WPI: 2001-211461/21.		
DR	N-PSDB: AAS02076.		
XX			
PT	New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's disease		
PT			
XX			
XX			
PS	Claim 8: Fig 22: 362pp: English.		
XX			
XX	The sequence represents the amino acid sequence of human TANGO 509 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunodeficiency syndrome), inflammatory disorders (e.g. psoriasis and asthma), renal disorders, embryonic disorders, brain-related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate-related disorders, pituitary-related disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's disease).		
CC			

XX SQ Sequence 290 AA:

Query Match 100.0%; Score 1511; DB 22; Length 290;
 Best Local Similarity 100.0%; Pred. No. 7.3e-135;
 Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRFAVFIEFTYWHLLNAFTVTPKDYVVEYGSNMITECKPFYERQDLALIVYWE 60
 |||||
 DB 1 mrlfavfilmywhllnaftvtpkdyvveysnmiteckfpevkdldlaalivyme 60

OY 61 DKNIIQFVHGEEEDLKVOHSSYRQARLKDQLSLGNAALQITVYKLDACVYRCMTSYG 120
 |||||
 DB 61 dknllqfvhgeedlkvqhsyrgarllkdqlslgnaalqitdvkldagvyrcmisyg 120

OY 121 ADVKRTIVVNAFYKINORILVDPVTSHELTQAEQPKAEVIMTSSDHQVLSGKTT 180
 |||||
 DB 121 advkrtivvnapynkinqrlivdpvtshelctqaegypkaevimtsdhvlsqkt 180

C 181 TTNSKREKLEFNTSTLRINTTTNEIFYCTFRRLDPEENHTAEVLVPELPLAHPNERTH 240
 |||||
 DB 181 ttnskreklfnvstlrlntttneifyctfrldepenhtaevlvpelplahpnerth 240

OY 241 LVTLGAILLCLGVALTFPRLRKGRMDVKKCGIOTNSKSGSDPHLEET 290
 |||||
 DB 241 lvtlgailliclgvaltflfrlrkgrmdvkkcgldtlnsksgsdphleet 290

RESULT 4
 AAY72677
 ID AAY72677 standard; Protein: 290 AA.
 XX AC AAY72677;
 XX DT 19-JUN-2001 (first entry)
 XX DE Human B7-4 membrane (B7-4M) protein.
 XX KW Human B7-4 membrane protein; B7-4M; receptor PD-1; chromosome 9; tumour;
 KW antiviral; anti-allergic; gene mapping; cytostatic; myocardial infarction;
 KW atherosclerosis; neurological disease; immunomodulatory; allergy; GVHD;
 KW graft-versus-host disease; immunosuppressive disease; organ transplant;
 KW acquired immune deficiency syndrome; AIDS; autoimmune disease; therapy.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FH Peptide 1..18
 FT /label= Signal_peptide
 FT Protein 19..290
 FT /label= Mature_B7-4M_protein
 FT Domain 19..134
 FT /label= IgV_domain
 FT Domain 19..238
 FT /label= Extracellular_domain
 FT Domain 135..227
 FT /label= IgC_domain
 FT Domain 239..259
 FT /label= Transmembrane_domain
 FT Domain 260..290
 FT /label= Cytoplasmic_domain
 XX WO200114557-A1.
 XX PD 01-MAR-2001.
 XX PF 23-AUG-2000; 2000WO-US23347.
 XX AC 23-AUG-1999; 99US-0150390.
 XX PR 10-NOV-1999; 99US-0164897.
 XX PA (DAND) DANA FARBER CANCER INST INC.

PA (GENY) GENETICS INST INC.
 XX PI Wood C, Freeman GJ;
 XX DR WPI, 2001-160116/16.
 XX DR N-PSDB: AAD02773.
 XX PT Treating e.g. cancer or allergies comprises contacting an immune cell
 PT with an agent that modulates signalling via PD-1 or B7-4 to modulate the
 PT immune response -
 XX Example 1; Fig 4; 168pp; English.
 XX The present sequence is human B7-4 membrane (B7-4M) protein having a
 CC transmembrane and short cytoplasmic domain. The human B7-4 cDNA is
 CC isolated from human activated keratinocyte and placental cDNA libraries.
 CC B7-4 gene is localised on human chromosome 9.
 CC The invention relates to a method for modulating immune response by
 CC contacting an immune cell with an agent that modulates signalling via
 CC B7-4 or its receptor PD-1. Modulating the interaction between PD-1 and
 CC B7-4 modulates a costimulatory or an inhibitory signal in an immune cell,
 CC resulting in the modulation of the immune response. The invention is
 CC useful for upregulating an immune response to treat tumours, neurological
 CC diseases and immunosuppressive diseases or to downregulate an immune
 CC response useful in organ transplants, graft-versus-host disease (GVHD),
 CC treating allergies and viral infections e.g., acquired immune deficiency
 CC syndrome (AIDS). The invention also provides B7-4 or PD-1 fusion proteins
 CC which are useful for treating immunological disorders, such as atherosclerosis
 CC diseases e.g., heart disease, myocardial infarction and atherosclerosis
 CC or in the case of inhibiting rejection of transplants. These fusion
 CC proteins are also used as immunogens to produce anti-B7-4 antibodies.
 CC PD-1 is useful in promoting the maintenance of pregnancy. B7-4 protein is
 CC highly expressed in placental trophoblasts and plays a role in preventing
 CC maternal rejection of the fetus. B7-4 cDNA is also useful for
 CC gene mapping.

XX SQ Sequence 290 AA:

Query Match 100.0%; Score 1511; DB 22; Length 290;
 Best Local Similarity 100.0%; Pred. No. 7.3e-135;
 Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRFAVFIEFTYWHLLNAFTVTPKDYVVEYGSNMITECKPFYERQDLALIVYWE 60
 |||||
 DB 1 mrlfavfilmywhllnaftvtpkdyvveysnmiteckfpevkdldlaalivyme 60

OY 61 DKNIIQFVHGEEEDLKVOHSSYRQARLKDQLSLGNAALQITVYKLDACVYRCMTSYG 120
 |||||
 DB 61 dknllqfvhgeedlkvqhsyrgarllkdqlslgnaalqitdvkldagvyrcmisyg 120

OY 121 ADVKRTIVVNAFYKINORILVDPVTSHELTQAEQPKAEVIMTSSDHQVLSGKTT 180
 |||||
 DB 121 advkrtivvnapynkinqrlivdpvtshelctqaegypkaevimtsdhvlsqkt 180

OY 181 TTNSKREKLEFNTSTLRINTTTNEIFYCTFRRLDPEENHTAEVLVPELPLAHPNERTH 240
 |||||
 DB 181 ttnskreklfnvstlrlntttneifyctfrldepenhtaevlvpelplahpnerth 240

OY 241 LVTLGAILLCLGVALTFPRLRKGRMDVKKCGIOTNSKSGSDPHLEET 290
 |||||
 DB 241 lvtlgailliclgvaltflfrlrkgrmdvkkcgldtlnsksgsdphleet 290

RESULT 5
 AAY72645
 ID AAY72645 standard; Protein: 290 AA.
 XX AC AAY72645;
 XX DT 31-MAY-2001 (first entry)
 XX DE Human B7-4 membrane (B7-4M) protein.

XX Human; B7-4 membrane protein; B7-4M; chromosome 9; antiviral; influenza;
 KW immunomodulatory; acquired immune deficiency syndrome; AIDS; anti-tumour;
 KW graft-versus-host disease; GVHD; immunological disorder; Herpes disease;
 KW autoimmune disease; common cold; shingles disease; encephalitis; therapy;
 KW organ transplant; gene mapping; transgenic; viral infection.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..18
 FT /label= Signal_peptide
 FT Protein 19..290
 FT /label= Mature_B7-4M_protein
 FT Domain 19..134
 FT /label= IGV_domain
 FT Domain 19..238
 FT /label= Extracellular_domain
 FT 135..227
 FT /label= IGC_domain
 FT 239..259
 FT Domain /label= Transmembrane_domain
 FT 260..290
 FT /label= Cytoplasmic_domain

W0200114556-A1.

01-MAR-2001.

23-AUG-2000; 2000WO-US23256.

23-AUG-1999; 99US-0150390.

(DAND) DANA FARBER CANCER INST. INC.

Freeman G, Bouslotis V, Chernova T, Malenkovich N;

WPI: 2001-202936/20.

N-PSDB; AAD02708.

PT New human B7-4 polypeptides useful for enhancing the immune response
 PT against a viral infection or induce a tumor immunity and to diagnose
 PT conditions related to aberrant B7-4 expression or activity

PS Claim 13; Fig 4; 123pp; English.

CC The present sequence is human B7-4 membrane (B7-4M) protein having a
 CC transmembrane and short cytoplasmic domain. Human B7-4 protein is
 CC isolated from human activated keratinocyte and placental cDNA libraries.
 CC B7-4 gene is localised on human chromosome 9.

CC The invention relates to human B7-4 secreted (B7-4S) protein, B7-4
 CC membrane (B7-4M) protein and their corresponding cDNA molecules. Human
 CC B7-4 proteins are useful for upregulating immune response to treat viral
 CC skin diseases such as Herpes disease or shingles disease, systemic viral
 CC diseases such as influenza, common cold and encephalitis, and for
 CC inducing tumor immunity or to downregulate an immune response useful in
 CC organ transplants, graft-versus-host disease (GVHD), treating allergies
 CC and viral infections e.g., acquired immune deficiency syndrome (AIDS).
 CC B7-4 antagonists are used to modulate the T cell co-stimulation by
 CC contacting an activated T cell with a B7-4 antigen. The invention is also
 CC used for producing non-human transgenic animals. It also provides B7-4
 CC fusion proteins which are useful for treating immunological disorders,
 CC such as autoimmune diseases or in the case of transplantation. B7-4
 CC fusion proteins are used as immunogens to produce anti-B7-4 antibodies.
 CC B7-4 cDNA is also useful for gene mapping. Methods are provided
 CC for modulating the immune response of individuals, by inhibiting or
 CC enhancing the lymphokine synthesis by the activated T cells. Diagnostic,
 CC prognostic, pharmacogenetics, screening and therapeutic methods are also
 CC provided using B7-4 proteins.

Sequence 290 AA;

Query Match 100.0%; Score 1511; DB 22; Length 290;
 Best Local Similarity 100.0%; Pred. No. 7,3e-135;
 Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIFAFTFMTYWHLLNMFYTVPRDLVYVEGSMNTECKEPVEKQLD...IYWEWE 60
 DB 1 mrlfavflfmywhllnlnftvprkdlvvegsnmnteckepvekdlaelivywene 60
 QY 61 DKNITGFVHGEEDLVQVSHSYRQARBLKQDLISGNAALQITDVKLDQAGVRCMISYGC 120
 DB 61 dknitgfvhgeedlvqvsyrrarllkqdlisgnaalqitdvkldqagvrcmlysgkc 120
 QY 121 ADYKRITKVNAPYKINORILVDPVSEHLETCOAGEPYKAEVIMVSSDHVSGKTT 180
 DB 121 adykritykvnaypynkinqrlivdpvsehelctqaegypkayevimvssdqhvysgktt 180
 QY 181 TTNSKREKLFNVSTFLRINTTNEIFVCTFRRLDPEENHTAEVLP...PLAHPPNERHT 240
 DB 181 ttnskreeklnfvstflrinttneifvctfrldpeenhtaejlpelplahppnerht 240
 QY 241 LVILGAILLCIGVALTFIFRLKRGKMDYKKCGIDPTNSKKOSDTHLEET 290
 DB 241 lvilgailcligvaltfifrlrkrgmmdykkcgldptnskkgsdthleet 290

RESULT 6

ID AAU01407 standard; Protein; 290 AA.

AC AAU01407;

DT 18-JUL-2001 (first entry)

XX Human TANGO 509, variant #1 amino acid sequence.

XX Human; TANGO 509; transmembrane protein; diagnostic; asthma;

XX immunological disorder; arthritis; graft rejection; renal disorder;

XX acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;

XX AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;

XX prostate; cerebrovascular disease; pituitary; Cushing's disease;

XX neurodegenerative disease; Parkinson's disease.

XX Homo sapiens.

OS W0200121631-A2.

PD 29-MAR-2001.

PF 20-SEP-2000; 2000WO-US25982.

PR 20-SEP-1999; 99US-0399723.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;

WPI: 2001-211461/21.

N-PSDB; AAS02118.

PT New nucleic acid encoding INTERCEPT 307, TANGO 511, TANGO 351, TANGO

PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful

PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's

PT disease -
 PS Disclosure: Page 344-345; 362pp; English.
 XX The sequence represents the amino acid sequence of human TANGO 509,
 CC variant #1 transmembrane protein. The nucleic acid and
 CC polypeptide sequences are useful for the diagnosis, prognosis and
 CC treatment of immunological disorders (e.g. arthritis, graft rejection and
 CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
 CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
 CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.

CC Ischaemia), tumours, prostate-related disorders, pituitary-related
CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
CC Parkinson's disease).

SO Sequence 290 AA:

Query Match 99.8%; Score 1508; DB 22; Length 290;
Best Local Similarity 99.7%; Pred. No. 1.4e-134;
Matches 289; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFAVFIFMTYWHLLNAFTVTPKDLVVEYGSNMTIECKFPVEKQJDLAALIVYEME 60
DB 1 mrlfavfifmtlywhllnaftvtpkdlvveygsnmtieckfpvekqjdlalivyweme 60
QY 61 DKNIOFVHGEEDLKVOHSSYRQARLLKQDLSGNALQITDVKLODAGVRCMISYGC 120
DB 61 dkniofvgheedlkvhssyrqarllkqqlsgnaalqitdvlkdagvrcmisygc 120
QY 121 ADYKRITVKNAPYKINQRIILVDPVTSHELTQCAEGYPKAEVITSSDHQVLSGKT 180
DB 121 adykritlevknaypnkinqrlilvdpvtshelctqageypkaevitssdhqylsgkkt 180
QY 181 TTNSKREELFNVTSTLRINTTNEIFCTFRRLDPEENHTAEVLVPELPLAPPNERTH 240
DB 181 ttnskreelkfnvstlrlnttneifctfrldpeenhtaelvlpelplappnerth 240
QY 241 LVILGAILLCLGVALTFFRLRGRMDVKKCGIODPNSKOSPTHLEET 290
DB 241 lvilgailllclgvalltffrlrgrmdvkkcgiodpnskkqsdthleec 290

RESULT 7

AAU01409 ID AAU01409 standard; protein; 290 AA.

AC AAU01409;

DT 18-JUL-2001 (first entry)

DE Human TANGO 509, variant #3 amino acid sequence.

XX Human; TANGO 509; transmembrane protein; diagnostic; asthma;
XX Immunological disorder; arthritis; graft rejection; renal disorder;
KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KM prostate; cerebrovascular disease; pituitary; Cushing's disease;
KM neurodegenerative disease; Parkinson's disease.

OS Homo sapiens.

PN WO200121631-A2.

PD 29-MAR-2001.

PF 20-SEP-2000; 2000WO-US25982.

PR 20-SEP-1999; 99US-0399723.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;

DR WPI; 2001-211461/21.

DR N-PSDB; AAS02120.

PT New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO
PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease -

Disclosure: Page 351; 362pp; English.

XX

CC The sequence represents the amino acid sequence of human TANGO 509,
CC variant #3 transmembrane protein. The nucleic acid and
CC polypeptide sequences are useful for the diagnosis, prognosis and
CC treatment of immunological disorders (e.g. arthritis, graft rejection and
CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.
CC ischaemia), tumours, prostate-related disorders, pituitary-related
CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
CC Parkinson's disease).

SO Sequence 290 AA:

Query Match 99.8%; Score 1508; DB 22; Length 290;
Best Local Similarity 99.7%; Pred. No. 1.4e-134;
Matches 289; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFAVFIFMTYWHLLNAFTVTPKDLVVEYGSNMTIECKFPVEKQJDLAALIVYEME 60
DB 1 mrlfavfifmtlywhllnaftvtpkdlvveygsnmtieckfpvekqjdlalivyweme 60
QY 61 DKNIOFVHGEEDLKVOHSSYRQARLLKQDLSGNALQITDVKLODAGVRCMISYGC 120
DB 61 dkniofvgheedlkvhssyrqarllkqqlsgnaalqitdvlkdagvrcmisygc 120
QY 121 ADYKRITVKNAPYKINQRIILVDPVTSHELTQCAEGYPKAEVITSSDHQVLSGKT 180
DB 121 adykritlevknaypnkinqrlilvdpvtshelctqageypkaevitssdhqylsgkkt 180
QY 181 TTNSKREELFNVTSTLRINTTNEIFCTFRRLDPEENHTAEVLVPELPLAPPNERTH 240
DB 181 ttnskreelkfnvstlrlnttneifctfrldpeenhtaelvlpelplappnerth 240
QY 241 LVILGAILLCLGVALTFFRLRGRMDVKKCGIODPNSKOSPTHLEET 290
DB 241 lvilgailllclgvalltffrlrgrmdvkkcgiodpnskkqsdthleec 290

RESULT 8

AAU01410 ID AAU01410 standard; protein; 290 AA.

AC AAU01410;

DT 18-JUL-2001 (first entry)

DE Human TANGO 509, variant #4 amino acid sequence.

XX Human; TANGO 509; transmembrane protein; diagnostic; asthma;
XX Immunological disorder; arthritis; graft rejection; renal disorder;
KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KM prostate; cerebrovascular disease; pituitary; Cushing's disease;
KM neurodegenerative disease; Parkinson's disease.

OS Homo sapiens.

PN WO200121631-A2.

PD 29-MAR-2001.

PF 20-SEP-2000; 2000WO-US25982.

PR 20-SEP-1999; 99US-0399723.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;

DR WPI; 2001-211461/21.

DR N-PSDB; AAS02121.

XX

PT New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO
PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease -
PS Disclosure; Page 354-355; 362pp; English.
XX
XX The sequence represents the amino acid sequence of human TANGO 509,
CC variant #4 transmembrane protein. The nucleic acid and
CC polypeptide sequences are useful for the diagnosis, prognosis and
CC treatment of immunological disorders (e.g. arthritis, graft rejection and
CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.
CC ischaemia), tumours, prostate-related disorders, pituitary-related
CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
CC Parkinson's disease).
XX
XX Sequence 290 AA;
SQ
Query Match 99.8%; Score 1508; DB 22; Length 290;
Best Local Similarity 99.7%; Pred. No. 1.4e-134;
Matches 289; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 MRIFVFRTMTWHLNATVTVPKDLVYVEGSMNTTECKRPVEKQDLALVYWEWE 60
DB 1 mlrlvflmlywhlnatlvtpkdlvveygsmntleckrpvqdlalvlyweme 60
OY 61 DKNIIQFVGEEDLVQVHSSYRQRRRLKDKQLSLGNAALQIDVYKLDAGVRCMISYGG 120
DB 61 dknllqfvggeedlvqvhssyrgrrrlldkqslsgnaalqidvkrldagvyrcmisygg 120
OY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHLTCQAESEYPAEVIWISSDQVLSGKTT 180
DB 121 adykriltvknvapykinqrllvdpvtseheltcqaesyphaevlwssdqvlsgktl 180
OY 181 TTNSKREKLFVWSTLRINTTNEIFYCTFRRRLDPEENHTAEVLPPLAHPPNERH 240
DB 181 ttnskreklfvwstlrlnttneifyctfrrrldpeenhtaelvlpplahppnerh 240
OY 241 LVILGAILLCGLVALTFIRLRKGRMDVKKGIQDTNSKOSDTHLEET 290
DB 241 lvilgailcglvaltfirllrkgrmdvkkcgldtnskqsdthleest 290
RESULT 9
AAE01222
AAE01222 standard; Protein; 290 AA.
AC AAE01222;
XX
XX 17-JUL-2001 (first entry)
XX
XX Human gene 1 encoded secreted protein allelic variant, SEQ ID NO:123.
DE
XX
XX Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiotensin disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnerability; gene therapy;
KW cell culture; chemotaxis; food additive; chromosome 9;
XX binding partner identification.
XX
XX Homo sapiens.
XX
XX WO200134768-A2.
XX
XX 17-MAY-2001.
PD

XX
XX 01-NOV-2000; 2000WO-US30039.
PF
XX
XX 09-NOV-1999; 9905-0164344.
PR
XX 07-APR-2000; 2000US-0195296.
PR
XX 27-JUL-2000; 2000US-0221367.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Olsen HS, Komatsoulis G, Duan DR, Ebner R, Kuben St,
PI WPI; 2001-308780/32.
DR
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure; Page 8; 474pp; English.
PS
XX
XX AAD05053-AAD05106 represent cDNAs corresponding to 15 human secreted
CC protein genes, and AAE01164-AAE01217 represent the proteins they encode.
CC AAE01218-AAE01226 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 15 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiotensin disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, to improve cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein allelic variant of B7-H6 protein referred to in the
CC disclosure of the invention.
XX
XX Sequence 290 AA;
SQ
Query Match 99.7%; Score 1507; DB 22; Length 290;
Best Local Similarity 99.7%; Pred. No. 1.7e-134;
Matches 289; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MRIFVFRTMTWHLNATVTVPKDLVYVEGSMNTTECKRPVEKQDLALVYWEWE 60
DB 1 mlrlvflmlywhlnatlvtpkdlvveygsmntleckrpvqdlalvlyweme 60
OY 61 DKNIIQFVGEEDLVQVHSSYRQRRRLKDKQLSLGNAALQIDVYKLDAGVRCMISYGG 120
DB 61 dknllqfvggeedlvqvhssyrgrrrlldkqslsgnaalqidvkrldagvyrcmisygg 120
OY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHLTCQAESEYPAEVIWISSDQVLSGKTT 180
DB 121 adykriltvknvapykinqrllvdpvtseheltcqaesyphaevlwssdqvlsgktl 180
OY 181 TTNSKREKLFVWSTLRINTTNEIFYCTFRRRLDPEENHTAEVLPPLAHPPNERH 240
DB 181 ttnskreklfvwstlrlnttneifyctfrrrldpeenhtaelvlpplahppnerh 240
OY 241 LVILGAILLCGLVALTFIRLRKGRMDVKKGIQDTNSKOSDTHLEET 290
DB 241 lvilgailcglvaltfirllrkgrmdvkkcgldtnskqsdthleest 290

Db 241 LVILGAILLCIGVALTFFILFRKGRMDVKKCGIQGDCNSKKQSDCHLEET 290

RESULT 10

ID AAU01408 standard; Protein: 290 AA.

AC AAU01408;

DT 18-JUL-2001 (first entry)

DE Human TANGO 509, variant #2 amino acid sequence.

XX

XX Human: TANGO 509; transmembrane protein; diagnostic; asthma;

KM immunological disorder; arthritis; graft rejection; renal disorder;

KM acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;

KM AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;

KM prostate; cerebrovascular disease; pituitary; Cushing's disease;

KM neurodegenerative disease; Parkinson's disease.

XX

XX Homo sapiens.

XX

XX WO200121631-A2.

XX

XX 29-MAR-2001.

XX

XX 20-SEP-2000; 2000WO-US25982.

XX

XX 20-SEP-1999; 99US-0399723.

XX

XX (MILL-) MILLENNIUM PHARM INC.

PI KIRST SJ, SHARP JD, FRASER CC, BARNES T, KINGSBURY G;

XX

XX WPI: 2001-211461/21.

XX

XX N-PSDB: AAS02119.

DR

DR New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO

PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful

PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's

PT disease -

XX

XX

PS Disclosure; Page 347-348; 362pp; English.

XX

XX The sequence represents the amino acid sequence of human TANGO 509,

CC variant #2 transmembrane protein. The nucleic acid and

CC polypeptide sequences are useful for the diagnosis, prognosis and

CC treatment of immunological disorders (e.g. arthritis, graft rejection and

CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.

CC psoriasis and asthma), renal disorders, embryonic disorders, brain-

CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.

CC ischaemia), tumours, prostate-related disorders, pituitary-related

CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.

CC Parkinson's disease).

XX

XX

SQ Sequence 290 AA;

Query Match 99.7%; Score 1507; DB 22; Length 290;

Best Local Similarity 99.7%; Pred. No. 1.7e-134;

Matches 289; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRIFAEIFMTYVHMLNAFTVTPKDYVVEYGSNMTIECKFPVEKQDLALIVYEME 60

Db 1 MRLIVFELMTYVHMLNAFTVTPKDYVVEYGSNMTIECKFPVEKQDLALIVYEME 60

QY 61 DKNIIFGVHGEEDIAKVSHSYRQARLLKQDLSGNALQITTVKLDAGVYRCMISYGC 120

Db 61 dknifgvhgeedikvshsyrfqrarllkqdlsgnalqitvkvldagvycrmisyyg 120

QY 121 ADVYRITVKNAPYKINORLIVDPYTSHELTGQABGYPKAEVITWSSHQLSGKTT 180

Db 121 adykrilvknapyknqrllivdpvtsehelcgaeypkacvltwssdhvylsgktc 180

QY 181 TTNSKREKLEFNWSTRIINTTNEIFVCTFRRLDPEENHTAEVLVPELPIAMPNFRTH 240

Db 181 ttnskreeklfenvstlrinntneifvctfrfldpeenhtaelvlpelplampnfrth 240

QY 241 LVILGAILLCIGVALTFFILFRKGRMDVKKCGIQDPTNSKKQSDPHLEET 290

Db 241 LVILGAILLCIGVALTFFILFRKGRMDVKKCGIQGDCNSKKQSDCHLEET 290

RESULT 11

AAE01219

ID AAE01219 standard; Protein: 235 AA.

AC AAE01219;

DT 17-JUL-2001 (first entry)

XX

XX Human gene 1 encoded secreted protein fragment, SEQ ID NO:120.

XX

XX Human: secreted protein; proliferative disorder; cancer; tumour;

KM foetal abnormality; developmental abnormality; haematopoietic disorder;

KM immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

KM inflammation; allergy; neurological disorder; Alzheimer's disease;

KM Parkinson's disease; cognitive disorder; schizophrenia; asthma;

KM skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;

KM cardiovascular disorder; angiotensin disorder; kidney disorder;

KM gastrointestinal disorder; pregnancy-related disorder;

KM endocrine disorder; infection; wound healing; vulnerability; gene therapy;

KM cell culture; chemotaxis; food additive; chromosome 9;

KM binding partner identification.

XX

XX Homo sapiens.

XX

XX WO200134768-A2.

XX

XX 17-MAY-2001.

XX

XX 01-NOV-2000; 2000WO-US30039.

XX

XX 09-NOV-1999; 99US-0164344.

PR 07-APR-2000; 2000US-0195286.

PR 27-JUL-2000; 2000US-0221367.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

PA

PI OLSEN HS, KOMATSUJIS G, DUAN DR, EDNER R, RUBEN SM;

XX

XX WPI: 2001-308780/32.

DR

DR Isolated nucleic acid molecule encoding a human secreted protein is

PT used in preventing, treating or ameliorating a medical condition -

PT

XX

XX

PS Disclosure; Page 8; 474pp; English.

XX

XX AAD05053-AAD05106 represent cDNAs corresponding to 15 human secreted

CC protein genes, and AAE01164-AAE01217 represent the proteins they encode.

CC AAE01218-AAE01226 represent human secreted protein fragments or variants.

CC The secreted proteins and their genes are useful for preventing,

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Pathological conditions can be diagnosed by determining the

CC amount of the new protein in a sample or by determining the presence of

CC mutations in the new genes. Specific uses are described for each of the

CC 15 genes, based on the tissues in which they are most highly expressed,

CC and include developing products for the diagnosis or treatment of

CC proliferative disorders, cancer, tumours, foetal and developmental

CC abnormalities, haematopoietic disorders, diseases of the immune system,

CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,

CC allergies, neurological disorders (e.g., Alzheimer's disease,

CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,

CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,

CC cardiovascular disorders, angiogenic disorders, kidney disorders,

DT	31-MAY-2001	(first entry)
XX		
DE	Human B7-4 secreted (B7-4S) protein.	
KW	Human; B7-4 secreted protein; B7-4S; chromosome 9; antiviral; influenza;	
KM	immunomodulatory; acquired immune deficiency syndrome; AIDS; anti-tumour;	
KW	graft-versus-host disease; GVHD; immunological disorder; Herpes disease;	
KW	autoimmune disease; common cold; shingles disease; encephallitis; therapy;	
KX	organ transplant; gene mapping; transgenic; viral infection.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..18
FT	Protein	/label= Signal_peptide
FT		19..245
FT		/label= Mature_B7-4S-protein
FT		/note= "Serves as an extracellular domain"
FT	Domain	19..134
FT		/label= IgV_domain
FT	Domain	135..227
FT		/label= IgC_domain
FT	Region	228..245
FT		/note= "Hydrophilic tail"
PN	WO200114556-A1.	
XX		
PD	01-MAR-2001.	
PF	23-AUG-2000; 2000WO-US23256.	
PR	23-AUG-1999; 99US-0150390.	
PA	(DAND) DANA FARBER CANCER INST INC.	
P1	Freeman G, Bousiotis V, Chernova T, Malenkovich N;	
DR	Freeze: 2001-202936/20.	
DR	N-PSDB; AAD02707.	
PT	New human B7-4 polypeptides useful for enhancing the immune response	
PT	against a viral infection or induce a tumor immunity and to diagnose	
PT	conditions related to aberrant B7-4 expression or activity	-
PS		
XX	Claim 13; Fig 3; 123pp; English.	
CC	The present sequence is human B7-4 secreted (B7-4S) protein having a	
CC	short hydrophilic tail without a membrane anchor or a transmembrane	
CC	domain. Human B7-4 protein is isolated from human activated keratinocyte	
CC	and placental cDNA libraries. B7-4 gene is localised on human	
CC	chromosome 9.	
CC	The invention relates to human B7-4 secreted (B7-4S) protein, B7-4	
CC	membrane (B7-4M) protein and their corresponding cDNA molecules. Human	
CC	B7-4 proteins are useful for upregulating immune response to treat viral	
CC	skin diseases such as Herpes disease or shingles disease, systemic viral	
CC	diseases such as influenza, common cold and encephalitis, and for	
CC	inducing tumour immunity or to downregulate an immune response useful in	
CC	organ transplants, graft-versus-host disease (GVHD), treating allergies	
CC	and viral infections e.g., acquired immune deficiency syndrome (AIDS).	
CC	B7-4 antagonists are used to modulate the T cell co-stimulation by	
CC	contacting an activated T cell with a B7-4 antigen. The invention is also	
CC	used for producing non-human transgenic animals. It also provides B7-4	
CC	fusion proteins which are useful for treating immunological disorders,	
CC	such as autoimmune diseases or in the case of transplantation. B7-4	
CC	fusion proteins are used as immunogens to produce anti-B7-4 antibodies.	
CC	B7-4 cDNA is also useful for gene mapping. Methods are provided	
CC	for modulating the immune response of individuals, by inhibiting or	
CC	enhancing the lymphokine synthesis by the activated T cells. Diagnostic,	
CC	prognostic, pharmacogenetics, screening and therapeutic methods are also	
CC	provided using B7-4 proteins.	
XX		
XQ	Sequence 245 AA:	

Query Match	Similarity	78.4%	Score 1184	DB 22	Length 245
Best Local	Similarity 100.0%	Pred. No. 5	1e-104		
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				Indels	0
				Gaps	0
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Db	1	mlfavlfaflfemcywhllnaftfvcpxkdluyveygsnmleackfvevkqdlafaiivymene	60		
QY	61	DKNIIOFVNGEEDLKVONHSSYRQRYRLRLKLDOLSLGNAALQITPDVKIOLVAGVRCGMISYGC	120		
Db	61	dknllqfghgeedlkvghssyqratarllkdqlslgnaalqitcdvklqddqgyrcmisygc	120		
QY	121	ADYKRITVKVNAFYKNQIRLLVVDPYTSEHELTCQAEQYPKAEYIWTSSDHQVLSGKTT	180		
Db	121	adykrltvcvnaqynkngirlvvdprvtsehelctqaeqyprkaeylwtssdhqvlsgktt	180		
QY	181	TNNSKREEKLFNVTSGLRINTNTTNNELFVCTPRRLDPEENHTKELVLP	227		
Db	181	tnnskreeklfmvtsclrlntnttnelvfctfrrldpeennhtkelp	227		

RESULT 14

ID AAE01179 standard; Protein; 245 AA.

AC AAE01179;

DT 17-JUL-2001 (first entry)

Human gene 1 encoded secreted protein HDPAP35, SEQ ID NO: 80.

KN Human; secreted protein; proliferative disorder; cancer; tumour;
 KN Foetal abnormality; developmental abnormality; haematopoietic disorder
 KN immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis
 KN inflammation; allergy; neurological disorder; Alzheimer's disease;
 KN Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KN skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KN cardiovascular disorder; angogenic disorder; kidney disorder;
 KN gastrointestinal disorder; pregnancy-related disorder; B7-H6 protein;
 KN endocrine disorder; infection; wound healing; vulnerrary; gene therapy;
 KN cell culture; chemotaxis; food additive; chromosome 9;
 KN binding partner identification.

OS Homo sapiens

FH	key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
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FT	/Label-mature_human_B7_H6-secreted_protein
1.0	1.0

FT /note= "Encoded by RGG"

PN W02001.34768-A2.

PD 17-MAY-2001.

PF 01-NOV-2000; 2000WO-US30039.

PR 09-NOV-1999; 99US-0164344.

PR 27-JUL-2000; 2000US-0221367.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Olsen HS, Komatsoulis G, Duan DR, Ebner R, Ruben SM;

DR WPI; 2001-308780/32.

XX

Oy 19 FTVAIVPKQLIYVVEGSSNNITTECKPVEKQLDLALITYVMEEDKN1IQFVIGSEEDLKVQH 78
Db 1 fttvvpkqllyvvegssnnitteckfpvekqldlaalilyvmeedkn1lqfivigseedlvkqh 60
Oy 79 SSYRRARLRLDQLSLGNAALQITDVKRLQDAGVYRCMISYGGAVYKRRITYVNVNPKYN 138

Db 61 syyqrarllkdglslnaalqlcdvklqdagyyrcmlsyg9adykrltvkvnaypnkin 120
QY 139 ORILVDPVPTSEHFLTCOAEGYPKAEVIMTSSDHQVLSGKTTTNSKREKLFNVTSTLR 198
Db 121 qrlivdpvlseneilcqaegypkaevlwcsdhqvlsqkcttcnskreeklfnvtcltr 180
QY 199 INTTNEIFYCTFRRRLDPEENHTAELVLPDLAAPP 235
Db 181 inttneifyctfrrldpeenhtaevlpeiplahpp 217

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Job time: 74 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 06:33:43 ; Search time 26.9 Seconds
(without alignments)
242.601 Million cell updates/sec

Title: US-09-649-108-1

Perfect score: 1511

Sequence: 1 MRFAVFIRMTYWHLLNAFT.....KCIQDPTNSKKSDTHLEET 290

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

1 number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177.5	11.7	306	2	US-08-147-772-4 Sequence 4, Appli
2	177.5	11.7	306	2	US-08-456-104-8 Sequence 8, Appli
3	177.5	11.7	306	2	US-08-101-624-25 Sequence 25, Appli
4	177.5	11.7	306	3	US-08-153-262-4 Sequence 4, Appli
5	177.5	11.7	306	3	US-08-479-744A-31 Sequence 31, Appli
6	177.5	11.7	306	4	US-08-280-757B-31 Sequence 31, Appli
7	177.5	11.7	306	4	US-09-159-135-4 Sequence 31, Appli
8	172	11.4	288	2	US-08-147-772-2 Sequence 4, Appli
9	172	11.4	288	2	US-08-456-104-6 Sequence 6, Appli
10	172	11.4	288	2	US-08-101-624-23 Sequence 23, Appli
11	172	11.4	288	3	US-08-153-262-2 Sequence 6, Appli
12	172	11.4	288	3	US-08-479-744A-29 Sequence 29, Appli
13	172	11.4	288	4	US-08-280-757B-29 Sequence 29, Appli
14	172	11.4	288	4	US-09-159-135-2 Sequence 2, Appli
15	172	11.4	288	4	US-08-205-697A-19 Sequence 19, Appli
16	172	11.4	288	4	US-08-702-525-19 Sequence 19, Appli
17	172	11.4	288	5	PCT-US95-02576-19 Sequence 19, Appli
18	172	11.4	288	5	PCT-US95-02576-17 Sequence 17, Appli
19	169.5	11.2	306	4	US-08-205-697A-17 Sequence 17, Appli
20	169.5	11.2	306	5	PCT-US95-02576-17 Sequence 17, Appli
21	169.5	11.2	306	5	PCT-US95-02576-12 Sequence 12, Appli
22	169.5	11.2	320	4	US-08-205-697A-12 Sequence 2, Appli
23	169.5	11.2	320	4	US-08-702-525-2 Sequence 2, Appli
24	169.5	11.2	320	5	PCT-US95-02576-2 Sequence 2, Appli
25	161.5	10.7	323	5	PCT-US94-09642-2 Sequence 2, Appli
26	161.5	10.7	329	2	US-08-456-104-2 Sequence 2, Appli
27	161.5	10.7	329	2	US-08-101-624-2 Sequence 2, Appli

28	161.5	10.7	329	3	US-08-479-744A-2 Sequence 2, Appli
29	161.5	10.7	329	4	US-08-280-757B-2 Sequence 2, Appli
30	161.5	10.7	329	4	US-08-205-697A-23 Sequence 23, Appli
31	161.5	10.7	329	4	US-08-702-525-23 Sequence 23, Appli
32	161.5	10.7	329	5	PCT-US95-02576-23 Sequence 23, Appli
33	158.5	10.5	208	3	US-08-630-172-15 Sequence 15, Appli
34	158.5	10.5	208	4	US-09-375-419-15 Sequence 15, Appli
35	156.5	10.4	473	4	US-09-171-945-131 Sequence 131, App
36	154.5	10.2	589	2	US-08-724-394A-1 Sequence 1, Appli
37	144	9.5	581	2	US-08-724-394A-3 Sequence 3, Appli
38	140	9.3	365	4	US-08-928-383B-2 Sequence 2, Appli
39	139.5	9.2	319	1	US-08-597-495B-22 Sequence 22, Appli
40	139.5	9.2	319	4	US-09-068-051A-22 Sequence 22, Appli
41	138	9.1	581	2	US-08-724-394A-2 Sequence 2, Appli
42	137	9.1	365	2	US-08-979-424-3 Sequence 3, Appli
43	137	9.1	365	4	US-09-272-456-2 Sequence 2, Appli
44	133.5	8.8	318	4	US-09-068-051A-32 Sequence 32, Appli
45	127.5	8.4	309	2	US-08-456-104-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-147-772-4
Sequence 4, Application US/08147772
Patent No. 5858776
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immune Reactivity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Mandagouras, Amy E.
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B lymphocyte activation antigen; Ig
DESCRIPTION: via activation of CD28 pathways, binds to, CD28+
DESCRIPTION: T cells, transmembrane protein
FEATURE:
NAME/KEY: signal sequence

APPLICANT: Nadler, Lee M.
 APPLICANT: Gray, Gary S.
 TITLE OF INVENTION: No. 5942607e1 CTLA4/CD28 Ligands and
 TITLE OF INVENTION: Uses Therefor
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/101,624
 FILING DATE: 26-JUL-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: RPT-004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 306 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 DESCRIPTION: B lymphocyte activation antigen; Ig
 DESCRIPTION: superfamily member; T cell costimulatory signal
 DESCRIPTION: via activation of CD28 pathways, binds to CD28+
 DESCRIPTION: T cells, transmembrane protein
 FEATURE:
 NAME/KEY: signal sequence
 LOCATION: -37 to -1
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 OTHER INFORMATION: hydrophobic
 FEATURE:
 NAME/KEY: extracellular domain
 LOCATION: 1 to 210
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: transmembrane domain
 LOCATION: 211 to 235
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: intracellular (cytoplasmic) domain
 LOCATION: 236 to 269
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: Ig V-set domain
 LOCATION: 1 to 105
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: Ig C-set domain
 LOCATION: 106 to 199
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 PUBLICATION INFORMATION:

AUTHORS: FREEMAN, GORDON J.
 AUTHORS: GRAY, GARY S.
 AUTHORS: GIMAT, CLAUDE D.
 AUTHORS: LOMBARD, DAVID B.
 AUTHORS: ZHOU, LIANG-JI
 AUTHORS: WHITE, MICHAEL
 AUTHORS: FINGEROTH, JOYCE D.
 AUTHORS: GRIEBEN, JOHN G.
 AUTHORS: NADLER, LEE M.
 TITLE: Structure, Expression, and T Cell Costimulatory
 TITLE: Activity Of The Murine Homologue Of The Human B
 TITLE: Lymphocyte Activation Antigen B7
 JOURNAL: Journal of Experimental Medicine
 VOLUME:
 ISSUE:
 PAGES:
 DATE: IN PRESS
 RELEVANT RESIDUES IN SEQ ID NO: 25: From -37 to 269
 US-08-101-624-25
 Query Match 11.7%; Score 177.5; DB 2; Length 306;
 Best Local Similarity 26.6%; Pred. No. 4.2e-10;
 Matches 57; Conservative 36; Mismatches 92; Indels 29; Gaps 11;
 QY 55 VYMEMEDKNIIOFVGEEDLKQVHSSYRQRARLLDQSLGNAALQITDVKLQDAGVRC 114
 DB 68 IYQKHDKVYLSVIAGK-LKV-WPEYKRT--LYDNTTY--SLILGLVLSDKGTSC 119
 QY 115 MI-----SYGADYKRTIVKVNAPYKINQRIILVDD--PYTSHELTQCOE-CYPAE 164
 DB 120 VQKKERGTGYVKHLALVKSIAKADFTSPN---ITSEGNPSADIKRITCFASGGFPAPR 175
 QY 165 VIVTSSDHOVLSGKTTTNSKREKLFNVSTLRINTTNEIFYCIPRRLLILENHTAE 224
 DB 176 FSWLENGRE-LPGINTTISQDESESLYTISSOLDENFTRNHTIKCLIKYGD--HVSBD 231
 QY 225 VPELPLAHPNERHIVITGAILICIGVALFEI 258
 DB 232 FTWEKPEDDPSKNTLVFGA---GFGAVITV 262
 RESULT 4
 US-08-153-262-4
 : Sequence 4, Application US/08153262
 : Patent No. 6071716
 : GENERAL INFORMATION:
 : APPLICANT: FREEMAN, GORDON J.
 : APPLICANT: FREEDMAN, ARNOLD S.
 : APPLICANT: NADLER, LEE M.
 : TITLE OF INVENTION: DNA Encoding B7, A New Member
 : TITLE OF INVENTION: OF The IgG Superfamily With Unique Expression On
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: The Dana-Farber Cancer Institute
 : STREET: 44 Binney Street
 : CITY: Boston
 : STATE: Massachusetts
 : COUNTRY: U.S.A.
 : ZIP: 02115
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
 : COMPUTER: IBM Personal System 2; Model 30
 : OPERATING SYSTEM: MS/DOS
 : SOFTWARE: WordPerfect 5.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/153,262
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/751,306
 : FILING DATE: 28-AUG-1991

```

1  ATTORNEY/AGENT INFORMATION:
2  NAME: HART, JULIA D.
3  REGISTRATION NUMBER: 33132
4  REFERENCE/DOCKET NUMBER: DFCI-116.1
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: (203) 255-8900
7  TELEFAX: (203) 259-2846
8  INFORMATION FOR SEQ ID NO: 4:
9  SEQUENCE CHARACTERISTICS:
10  LENGTH: 306 amino acids
11  TYPE: amino acid
12  TOPOLOGY: linear
13  MOLECULE TYPE: protein
14  DESCRIPTION: B lymphocyte activation antigen; Ig
15  DESCRIPTION: superfamily member; T cell costimulatory signal
16  DESCRIPTION: via activation of CD28 pathways, binds to CD28+
17  DESCRIPTION: T cells, transmembrane protein
18  FEATURE:
19  NAME/KEY: signal sequence
20  LOCATION: -37 to -1
21  IDENTIFICATION METHOD: similarity with known
22  IDENTIFICATION METHOD: sequence
23  OTHER INFORMATION: hydrophobic
24  FEATURE:
25  NAME/KEY: extracellular domain
26  LOCATION: 1 to 210
27  IDENTIFICATION METHOD: similarity with known
28  IDENTIFICATION METHOD: sequence
29  FEATURE:
30  NAME/KEY: transmembrane domain
31  LOCATION: 211 to 235
32  IDENTIFICATION METHOD: similarity with known
33  IDENTIFICATION METHOD: sequence
34  FEATURE:
35  NAME/KEY: intracellular (cytoplasmic) domain
36  LOCATION: 236 to 269
37  IDENTIFICATION METHOD: similarity with known
38  IDENTIFICATION METHOD: sequence
39  FEATURE:
40  NAME/KEY: Ig V-set domain
41  LOCATION: 1 to 105
42  IDENTIFICATION METHOD: similarity with known
43  IDENTIFICATION METHOD: sequence
44  FEATURE:
45  NAME/KEY: Ig C-set domain
46  LOCATION: 106 to 199
47  IDENTIFICATION METHOD: similarity with known
48  IDENTIFICATION METHOD: sequence
49  UBLICATION INFORMATION:
50  AUTHORS: FREEMAN, GORDON J.
51  AUTHORS: GRAY, GARY S.
52  AUTHORS: GIMMI, CLAUDE D.
53  AUTHORS: LOMBARD, DAVID B.
54  AUTHORS: ZHOU, LIANG-JI
55  AUTHORS: WHITE, MICHAEL
56  AUTHORS: FINGEROTH, JOYCE D.
57  AUTHORS: GRIBBEN, JOHN G.
58  AUTHORS: NADLER, LEE M.
59  TITLE: Structure, Expression, and T Cell Costimulatory
60  TITLE: Activity Of The Murine Homologue Of The Human B
61  TITLE: Lymphocyte Activation Antigen B7
62  JOURNAL: Journal of Experimental Medicine
63  VOLUME:
64  ISSUE:
65  PAGES:
66  DATE: IN PRESS
67  RELEVANT RESIDUES IN SEQ ID NO: 4: From -37 to 269
68  US-08-153-262-4
69  Query Match 11.7%; Score 177.5; DB 3; Length 306;
70  Best Local Similarity 26.6%; Pred. No. 4.2e-10;
71  Matches 57; Conservative 36; Mismatches 92; Indels 29; Gaps 11.

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01 55 YWMEHEDNIIIOFNVEEDLIVYOHSSYRQARLLIKDLSGNMALTOTTDVKLDDAGCYRC 114
02 68 IYWKQHKDKVYLSTYAGK--LKV-WPEYKRNRT--LYDWTY---SLIILGLVLI-SDRGTYSC 119
03 115 MI-----SYGADYKRYTVKVNAPYKINQRIILVVD--PVTSEHETGQAR-GYPAKE 164
04 120 VQKKERCTGYCVKHLALVKLISKADFSTPN---ITSCGNPSADYKKITVCFASGCFPR 179
05 126 FSWLENGRE-LPGINVTITSDPESELVTITSSQDLENFTTRNHTIKCLAKYGDG--HVS 231
06 225 VIPELPLAHPNERTHLVILCAIILLCGLVATFI 258
07 232 FTWKKRPEDPPDSKNTLVLFPA---GGAVITTV 262
08 RESULT 5
09 : Sequence 31, Application US/08479744A
10 : Patent No. 6084067
11 :
12 : GENERAL INFORMATION:
13 :
14 : APPLICANT: Freeman, Gordon J.
15 : APPLICANT: Nadler, Lee M.
16 : APPLICANT: Gray, Gary S.
17 : TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
18 : TITLE OF INVENTION: Uses therefor
19 : NUMBER OF SEQUENCES: 55
20 : CORRESPONDENCE ADDRESS:
21 : ADDRESSEE: LAHIVE & COCKFIELD, LLP
22 : STREET: 60 State Street
23 : CITY: Boston
24 : STATE: Massachusetts
25 : COUNTRY: USA
26 : ZIP: 02109
27 :
28 : COMPUTER READABLE FORM:
29 : MEDIUM TYPE: floppy disk
30 : COMPUTER: IBM PC compatible
31 : OPERATING SYSTEM: PC-DOS/MS-DOS
32 : SOFTWARE: PatentIn Release #1.0, Version #1.25
33 :
34 : CURRENT APPLICATION DATA:
35 : APPLICATION NUMBER: US/08/479,744A
36 : FILING DATE: June 7, 1995
37 : CLASSIFICATION: 435
38 :
39 : PRIOR APPLICATION DATA:
40 : APPLICATION NUMBER: 08/280,757
41 : FILING DATE: 26-JUL-1994
42 : APPLICATION NUMBER: 08/109,393
43 : FILING DATE: 28-AUG-1993
44 : APPLICATION NUMBER: 08/101,624
45 : FILING DATE: 26-JULY-1993
46 : APPLICATION NUMBER: 08/147,773
47 : FILING DATE: 3-NOV-1993
48 :
49 : ATTORNEY/AGENT INFORMATION:
50 : NAME: Mandragouras, Amy E.
51 : REGISTRATION NUMBER: 36,207
52 : REFERENCE/DOCKET NUMBER: RPI-004CP3
53 : TELECOMMUNICATION INFORMATION:
54 : TELEPHONE: (617) 227-7400
55 : TELEFAX: (617) 227-5941
56 :
57 : INFORMATION FOR SEO ID NO: 31:
58 : SEQUENCE CHARACTERISTICS:
59 : LENGTH: 306 amino acids
60 : TYPE: amino acid
61 :
62 : TOPOLOGY: linear
63 :
64 : MOLECULE TYPE: protein
65 : DESCRIPTION: B lymphocyte activation antigen; Ig
66 : DESCRIPTION: superfamily member; T cell costimulator; signal
67 : DESCRIPTION: via activation of CD28 pathways, binds to CD28+
68 : DESCRIPTION: T cells, transmembrane protein
69 :
70 : FEATURE:
71 : NAME/KEY: signal sequence

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NAME/KEY: Ig V-set domain
LOCATION: 1 to 105
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 106 to 199
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: GRAY, GARY S.
AUTHORS: GIMMI, CLAUDE D.
AUTHORS: LOMBARD, DAVID B.
AUTHORS: ZHOU, LIANG-JI
AUTHORS: WHITE, MICHAEL
AUTHORS: FINGEROTH, JOYCE D.
AUTHORS: GRIBBEN, JOHN G.
AUTHORS: NADLER, LEE M.
TITLE: Structure, Expression, and T Cell Costimulatory
TITLE: Activity of The Murine Homologue Of The Human B
JOURNAL: Journal of Experimental Medicine
VOLUME:
ISSUE:
PAGES:
DATE: IN PRESS
RELEVANT RESIDUES IN SEQ ID NO: 31: From -37 to 269
US-08-280-757B-31

Query Match 11.7%; Score 177.5; DB 4; Length 306;
Best Local Similarity 26.6%; Pred. No. 4.2e-10;
Matches 57; Conservative 36; Mismatches 92; Indels 29; Gaps 11;

QY 55 VYMEEDKNIIFVHGDEPKVQSSYRORARLKLDLSGNALQITDYLQDAGYRC 114
DB 68 IYWKHKDVVSLVAGK-LKV-WPEYKNT--LYDNTT---SLILGLVLSRGYISC 119
QY 115 MI-----SYGADYKRITVKNAPYKINORILVVD---PVTSEHETLCOAE-GYPRAE 164
DB 120 VVQKKEGTGKHLALVKLSIKADFSPN---ITSGNSADTKRTCTCAGSGFPKPR 175
QY 165 VIVTSSDHOVLSCGTTTNSKREKLENVTSLKINTTNEIFCTRRRLDPENHIAEL 224
DB 176 FSWLENGRE-LPGINTTISODPESELYTSSQIDFNTRHTIKLKYGDA---HVSDE 231
QY 225 VPELPPLAHPPNERTHLYILGAILLCGVALTFI 258
DB 232 FTWEKPPEDPPDSKNTLVFGA---GFGAVITTV 262

RESULT 7
US-09-159-135-4
Sequence 4: Application US/09159135
Patent No. 6149905
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells with Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B lymphocyte activation antigen; Ig
DESCRIPTION: superfamily member; T cell costimulatory signal
DESCRIPTION: via activation of CD28 pathways, binds to CD28+
DESCRIPTION: T cells, transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -37 to -1
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 210
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 211 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular (cytoplasmic) domain
LOCATION: 236 to 269
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 105
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 106 to 199
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: GRAY, GARY S.
AUTHORS: GIMMI, CLAUDE D.
AUTHORS: LOMBARD, DAVID B.
AUTHORS: ZHOU, LIANG-JI
AUTHORS: WHITE, MICHAEL
AUTHORS: FINGEROTH, JOYCE D.
AUTHORS: GRIBBEN, JOHN G.
AUTHORS: NADLER, LEE M.
TITLE: Structure, Expression, and T Cell Costimulatory
TITLE: Activity of The Murine Homologue Of The Human B
JOURNAL: Journal of Experimental Medicine
VOLUME:

ISSUE:
PAGES:
DATE: IN PRESS
RELEVANT RESIDUES IN SEQ ID NO: 4: From -37 to 269
US-09-139-135-4

Query Match 11.7%; Score 177.5; DB 4; Length 306;
Best Local Similarity 26.6%; Pred. No. 4.2e-10;
Matches 57; Conservative 36; Mismatches 92; Indels 29; Gaps 11;

QY 55 YVEMEDKNIIOFVGEEDLVKVOHSSYRORARLKDQSLGNAALQITPVKLDAGVYRC 114
DB 68 IYMKHDKVLSVIAKG--LKV-MPEYKVRT--LYDNFTY---SLIIIGLVISDRCTYSC 119
QY 115 MI-----SYGADYKRITVKNAPRNKINQILVVD---PVTSEHLTCQAE-GYPRAE 164
DB 120 VQKREKRGTYGVKHLALVLSIKADFSPN---ITSGNPADTKRKRTCFASGCFPKPR 175
QY 165 VMTSSDHQVLSGKTTTTSKREKLEFNTSTLRITNTNEIFCYCFRRLDEENTAEEL 224
DB 176 FSWLENGRE-LPGINTTISQDEPESELYTTSQLDRTTNNHTIKLIKYGDA---HVSSED 231
QY 225 VPELPPLAHPNRRHVLVILGAILLGLVALTFI 258
DB 232 FTWEKPPEDPPDSKNTLVLFGA---GFGAVITIV 262

RESULT 8
US-08-147-772-2

Sequence 2, Application US/08147772

Patent No. 5858776

GENERAL INFORMATION:

APPLICANT: Ostrand-Rosenberg, Suzanne

APPLICANT: Baskar, Sivasubramanian

APPLICANT: Glimcher, Laurie H.

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,772

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: B cell activation antigen; natural ligand

DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

FEATURE:

NAME/KEY: signal sequence

LOCATION: -34 to -1

IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein

OTHER INFORMATION: hydrophobic

FEATURE:

NAME/KEY: extracellular domain

LOCATION: 1 to 208

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: transmembrane domain

LOCATION: 209 to 235

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: intracellular domain

LOCATION: 236 to 254

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 19 to 21

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 55 to 57

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 152 to 154

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 177 to 179

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 192 to 194

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 198 to 200

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig V-set domain

LOCATION: 1 to 104

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

PUBLICATION INFORMATION:

4

; ATTORNEY/AGENT INFORMATION:
;
; NAME: Mandragouras, Amy E

4


```

REGISTRATION NUMBER: 36, 207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known

```

```

IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic T Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 6
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262
US-08-101-624-23

Query Match      11.4%: Score 172; DB 2; Length 288;
Best Local Similarity 22.1%; Pred. No. 1.4e-09;
Matches 58: Conservative 56; Mismatches 97; Indels 52; Gaps 12;

25 KDLYVEGSMNTTICKRPFPEKQDLALIVYMEDKNIIIDFVGCEBDLKVOSSYHOR 84
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
43 KEVALISCGHNVSE-----ELAQTRIMQEKKKMVLTMMSGDMINIREYN----- 89
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
85 ARLLKDQLSLGNALQIIDVKLQDAGVRCMI-STYGADYKR-----IIVKNAPYRK 136
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
90 -RTIPD--ITNNLSIVIALRPDSDEGTVCVLAKDKAFKEHLAEVTLSYKADFPPPS 146
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
137 INORLIYVDPTYSHELTCQAE-GYKRAEVITWSSDHQVLSKPTMTTSKREKLFNVT 195
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
147 ISDFE---PTSNIIRRICSTSGCFEPHLSLENGEE-LNAINTTVSJDIFTELAVSS 202
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
196 FLRIINTTNEIFYC-----TFRRRLPEENHTAELVIPLEPLAHPPERTHALVL 244
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
203 KLDPMWTNNHSPMLCKIKYGLRVNQTFMMWNTTKQHPRDNILLPSVAI-----I 255
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
245 GAILLCGLVALFTF-RLRGR 265
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
256 GFVVIC---CLTYCAPRCRERR 275
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 11
US-08-751-767A-6
Sequence 6, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLOBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
U-751-767A-6

Query Match 11.48; Score 172; DB 2; Length 288;
Best Local Similarity 22.18; Pred. No. 1,4e-09;
Matches 58; Conservative 56; Mismatches 97; Indels 52; Gaps 12;

QY 25 KDLVVEGSGMTIECFPEYKQDLALAIYWMEDKNIQFVHGEEDLKVOHSSYROR 84
D 43 KEVATLSCGHVSYE-----ELAOTRIYMKKKMTLMSGDMINPEKRN----- 89
QY 85 ARLLKDLISGNAALQITDVKLDAGVYRCMI-SYGGADYKR-----ITVKVAPYRK 136
D 90 -RTTFD--ITNNLSIVILALRPSDEGTVECVLKEKDAFKREHLAEVTLVKADFPPT 146
QY 137 INQILLVADPTSHSLTLCQAE-GYPRAEVITWSSDHQVLSGKTTTNSKREKLEFNTS 195
D 147 ISDEIT--PTSNIRRICTSGGPEPHLSWLENGEE-LNAINTVTSODEPTELYAVSS 202
QY 196 TLRINTTNEIFYC-----TFRRLDPENHTAEVLVPELPLAHPPNERTHVL 244
D 203 KLDPMNTNHSFMCILIKYGLRVNQTFMWNNTKQEHFNDNLPSMAI-----TLISVN 255
QY 245 GAILLCGLVALTFIF--RLRGR 265
D 256 GIFVIC--CLTYCFAPRCRERR 275

R-12
US-09-649-153-262-2
Sequence 2, Application US/08153262
Patent No. 6071716
GENERAL INFORMATION:
APPLICANT: FREEMAN, GORDON J.
APPLICANT: FREEDMAN, ARNOLD S.
APPLICANT: NADLER, LEE M.
TITLE OF INVENTION: DNA Encoding B7, A New Member
TITLE OF INVENTION: Of The IgG Superfamily with Unique Expression On
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Dana-Farber Cancer Institute
STREET: 44 Binney Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM Personal System 2; Model 30
OPERATING SYSTEM: MS/DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,262
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 35 to 37
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:

NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEDMAN, GORDON J.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-153-262-2

Query Match 11.4%; Score 172; DB 3; Length 288;
Best Local Similarity 22.1%; Pred. No. 1.4e-09;
Matches 58; Conservative 56; Mismatches 97; Indels 52; Gaps 12;

QY 25 KDLVVEYSGNNTICKPEVKQDLALIVYEMEDKNIIOFVHGEDLKVOHSSYROR 84
DB 43 KEVALTSCGHNVSV-----ELAQTRITWKEKKVMTVMMSGDMNIMPEYKN---- 89
QY 85 ARLKDOJSLGNAALQITDVKLDAGVYRCMT-SYGGADYK-----ITKVNAPIYK 136
DB 90 -RTIPD--ITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADFPPTS 146
QY 137 INORILVDPVSEHELTQAE-GYKAEVITWSSDHQVLSGKTTTNSKREKLEFNVS 195
DB 147 ISDFEIT--PNSNIRRIICSTSGFPEPLSLWLENGEE-LNAINTTVSODPETELXAVSS 202
QY 196 TLRIINTTNEIFYC-----TFRRLDPEENHTAELVIPLELPAHPNERHVLVL 244
DB 203 KLDFNMNTNHSFMCILKYGHLELVNOTFNWNTYKQEHFPDNLPSVAL-----TLISVN 255
QY 245 GAILLCGLVALFTF--RLRKGR 265
DB 256 GIEVIC---CLTYCFAPRCRERR 275

RESULT 13
US-08-479-744A-29
Sequence 29, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation


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Query March 11.4%: Score 172: DB 4: Length 288:
Best Local Similarity 22.1%: Pred. No. 1.4e-09:
Matches 58: Conservative 56: Mismatches 97: Indels 52: Gaps 12:

QY 25 KDLVVEYGSMMTECKRPVEKODIALLIYWEMEDKNIIQDFVHGEPDLKVKQSSYRQR 84
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 43 KEVATLSGCHNVSE-----ELAQTRIVYQKQKKMVLTMNSGDMNIMREYN----- 89
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 85 ARLLKQDLSLGNALQITDVKLDAGVYRCMI-STGGADYKR-----ITYKVAAPYRK 136
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 90 -RTIFD--ITNNLSIVILALRPSDEGTVECVLKEKDAFKREHLAEVTLISKADFPPTPS 146
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 137 INQRLVADPTSHSELTLQCAE-GYPRKAEVITSSDQVLGSKTPTTSKREKLFNTS 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 147 ISDEI---PYSNLRRIICSTSGGEPHLSLLENGEE-LNAINTVVSQDPTELYAVSS 202
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 196 TLRINTTNEIFYC-----TFRRLDPEENHTAEVLVPELPALHPPERTHLVIL 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 KLDFMTWTNHSFMCILKXGLHVRNGTFMNTTKQHPFDNLPSVAI--- -TLISVN 255
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 GAILLCGLVALTEF--RLRKGR 265
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 256 GIFVIC---CLTYCFAPRCRERR 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-09-159-135-2
: Sequence 2, Application US/09159135
: Patent No. 6149905
: GENERAL INFORMATION:
: APPLICANT: Ostrand-Rosenberg, Suzanne
: APPLICANT: Baskar, Sivasubramanian
: APPLICANT: Glimcher, Laurie H.
: APPLICANT: Freeman, Gordon J.
: APPLICANT: Nadler, Lee M.
: TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street, Suite 510
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/159,135
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/147,772
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Mandragouras, Amy E.
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: RPI-003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 288 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: DESCRIPTION: B cell activation antigen; natural ligand
: FEATURE: for CD28 T cell surface antigen; transmembrane protein

```

```

NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.

```

1
 2 AUTHORS: SEGIL, JEFFREY M.
 3
 4 AUTHORS: LEE, GRACE
 5
 6 AUTHORS: WHITMAN, JAMES F.
 7
 8 AUTHORS: NADLER, LEE M.
 9
 10 TITLE: B7, A New Member Of The Ig Superfamily With
 11
 12 TITLE: Unique Expression On Activated And Neoplastic B Cells
 13
 14 JOURNAL: The Journal of Immunology
 15
 16 VOLUME: 143
 17
 18
 19 ISSUE: 8
 20
 21 PAGES: 2714-2722
 22
 23 DATE: 15-OCT-1989
 24
 25 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 26
 27 US-09-159-135-2

[illegible]

Search completed: March 18, 2002, 06:35:53
Job time: 130 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2002, 06:33:43 ; Search time 37.45 Seconds
(without alignments)
589.870 Million cell updates/sec

Title: US-09-649-108-1

Perfect score: 1511

Sequence: 1 MRFVAFIMTYMHLNAFT.....KCGIDPTNSKQSDTHLEET 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

T number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR-68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	12.2	487	2 S65133	butyrophilin - mou
2	174	11.5	526	2 A37821	butyrophilin - bov
3	172	11.4	288	2 A45803	B-cell-restricted
4	169.5	11.2	309	2 I49503	B-lymphocyte activ
5	169	11.2	526	2 S70587	butyrophilin precu
6	165	10.9	289	2 G00031	B7 protein - red-c
7	162	10.7	299	2 I46690	CD80 precursor - r
8	161.5	10.7	329	1 A48754	B7-2 antigen - hum
9	161	10.7	330	2 I46691	CD86 precursor - r
10	156	10.3	321	2 I54766	B-lymphocyte activ
11	134	8.9	391	2 T09058	butyrophilin homol
12	132	8.7	853	1 IJBOHC	neural cell adhesi
13	130	8.6	1088	1 IJXJNL	neural cell adhesi
14	129	8.5	725	1 JE0099	neural cell adhesi
15	128	8.5	725	1 JE0100	neural cell adhesi
16	128	8.5	1092	1 JN0635	neural cell adhesi
17	127.5	8.4	309	2 I49522	gene B7-2 protein
18	126	8.3	1106	1 PFHUGB	platelet-derived g
19	126	8.3	5175	2 T20992	hypothetical prote
20	126	8.3	5198	2 T43290	hemiscentin precurs
21	122	8.1	761	1 IJHUNG	neural cell adhesi
22	122	8.1	1028	1 A53449	plasmacytoma-assoc
23	121.5	8.0	1338	2 S09982	protein-tyrosine k
24	120.5	8.0	646	2 I38042	cell surface glyco
25	118.5	7.8	587	2 JH0464	DM-GRASP precursor
26	118.5	7.8	588	2 JH0506	adhesion molecule
27	118	7.8	725	1 IJMSNG	neural cell adhesi
28	118	7.8	1115	1 IJMSNL	neural cell adhesi
29	117.5	7.8	2132	1 A55182	agrecan precursor

30	117	7.7	1091	1 IJCHNL	neural cell adhesi
31	116.5	7.7	243	2 I51746	myeloid class II alpha
32	116.5	7.7	370	2 S29139	agrecan - pig (fr
33	116.5	7.7	588	2 A45234	surface glycoprote
34	116.5	7.7	1427	2 I51669	tyrosine phosphor
35	115.5	7.6	333	2 A31923	adhesion protein pr
36	115	7.6	946	1 A47299	myeloid protein pr
37	115	7.6	1336	2 I60598	myeloid tyrosine kin
38	114.5	7.6	2415	1 A39086	neural precursor
39	114	7.5	818	2 IJ9120	hypothetical prote
40	114	7.5	858	1 IJRTNC	neural cell adhesi
41	113	7.5	1033	2 S19247	cell adhesion prot
42	112.5	7.4	7962	2 I38346	elastic titin - hu
43	112	7.4	1028	2 I58164	Big-1 protein - ra
44	111.5	7.4	538	2 J52457	vascular cell adhe
45	111.5	7.4	1018	2 J54211	neural adhesion pr

ALIGNMENTS

RESULT 1
S65133
butyrophilin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999

C:Accession: S65133
R:Smith, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 285-292, 1995
A:Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically assoc
A:Reference number: S65133; MUID:96125722
A:Accession: S65133
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-487 <ISH>
A:Cross-references: GB:S80642; NID:g1246078; PIDN:AAB35893.1; QID:g1246079

Query Match 12.2% Score 185; DB 2: Length 147;
Best Local Similarity 25.7%; Pred. No. 6e-07;
Matches 62; Conservative 45; Mismatches 120; Indels 14; Gaps 6;

QY	38	IECKPVEKQDLALIVYEMEDKRIIOFVHGEEDLKVQSHSYRCRAVLTKDQSLGNA	97
DB	12	LTCGSPNASSFYMLMFRQTRSTAVLIXRQGEDEGQMTREGRATLALAGLIDGRA	71
QY	98	ALQITDVKLQAGVYRCMISYGADYKRTYKVNAPYKINQRIIVDPVTSHELTQCA	157
DB	72	TLIRIDVRFSDGGEYRCLFK-DNDPFEENAVYLKVAAGSDPOISMTVQEMCMELECTS	130
QY	158	EG-YKAEVYMTSSDHOVLSGKTTTNSKR--EKLFNVTSLKRIINTTNEIFYCTFRLL	214
DB	131	SCWYEPQVQMTGNREML---PSTSDSKHNEEGLEFVAVSMISDSSIA--MSCCIONI	187
QY	215	DEEHNFAELVPELPLAHPNERHVLIGAILLCLIGV---ALCTFPLPQKGRMDVK	270
DB	168	LLGQCKEVDI---SLPAPVPRALPTPIYAVATITLALGLTLGSIFFWKLIYKSSSLRK	244
QY	271	K 271	
DB	245	K 245	

RESULT 2
A37821
butyrophilin - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
C:Accession: A37821
R:Jack, L.J.W.; Mather, I.H.
J. Biol. Chem. 265, 14481-14486, 1990
A:Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycopr

Oy 166 IWTSSDHVLSGKTKTTTNSKREELFVNTSLRINTTNELPOTFERLRDPEENHAEV 225
Db 177 SMLENGRE-LGINTTTISQDESESLYTIISOLDENTRNTTKICLIRYGA---HVSDEF 232
Oy 226 IPELPPLAHPNERTHVLVILGAILCLGVALTFI 258
Db 233 TWKRPEDPDSKNTLVLFGA--GFGAVITVV 262

RESULT 5
S70587
butyrophilin precursor - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S70587
R:Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Coueto, J.R.
Biochim. Biophys. Acta 1306, 1-4, 1996
A:Title: Cloning and sequence analysis of human butyrophilin reveals a potential receptor
A:Reference number: S70587; MUID:96201696
A:Accession: S70587
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-526 <TAY>
A:Cross-references: EMBL:U03576; NID:91326082; PIDN:AMC50489.1; PID:q1326083

Query Match	11.28	Score 169	DB 2	Length 526
Best Local Similarity	25.28	Pred. NO. 1.2e-05		
Matches 64	Conservative 44	Mismatches 132	Indels 14	Gaps 7

QY	19	FTYVYPKDLYVVEGSMNTICKPVRKQDLDLALIVYWEEMKNNIQFVH--GEEDLKV	76
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
Db	29	FDVIGPFPPIILAVNGEDAEIPLCR--LSPMSAEHELRLMRKKKSPAVLVNHRGREDDEAE	86
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
QY	77	QHSSTRQARILLKQDLSIGNAALDITDVKLDQAGVYRCMTSYSGADYKRITTVKNAEPYNK	136
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
Db	87	QMPERGRATLVQDGIKAGVVALRIRGVSDDEEYTCFPRFEDS--YEELVHLTKVALG	145
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
QY	137	INORLLVDPVTSSEHLTICOAEQ--YPRAEVLTWTSDDHQVLSGKTTTNSRKEELFVTS	195
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
Db	146	SDPHSMQVOENGELCLECTSVGMYPEPQYOMRTSKKEKRP--STSESRNDEEGILFTVA	204
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
QY	196	TLRIINTTNEIFYCTFRRLDEENHTAEVLIPELPLAHPNERTHLLVIGALLILGCV--	253
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
Db	205	SVIIRDTSTKNVNCYIQLNLLLGQKKVEISIPASL--PRLPPIVAVAVALVILVIGLLT	261
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
QY	254	--ALTFIRLAKGR	265
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	
T	262	IGSIFETWRLYNER	275
		1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32	

RESULT 6
G00031
B7 protein - red-crowned mangabey (fragment)
C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031
R:Villinger, F.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: G00217
A:Accession: G00031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <VIL>
A:Cross-references: EMBL:U19833; NID:G644783; PIDN:AAAB6700.1; PID:G644784
C:Genetics:
A:Gene: B7
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match	10.9%	Score 165;	DB 2;	Length 289;
Best Local Similarity	22.1%	Pred. No. 1.1e-05;		
Matches 58;	Conservative 55;	Mismatches 98;	Indels 52;	Gaps 12;

```

Oy      25 KDLVVEGSGMTECKFPVEKODLALIVYEMGEKNTIOGVHGEDILKVOHSSYROR  84
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      43 KEVATLSGHNVSVE-----ELAQTRIOCKEKKAMVLTMISGDMMNWPYKX-----  89

Oy      85 ARLKLDLSLGNALQITDYVKLODAGVYRCMI-SYGADYKR-----ITYKVNAPYK  136
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      90 -RTIFD--ITNNLSIVIALPSPDEGVECVULKEYEDAKREHLAEVMSVYADFPFS  146
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy      137 INORILVDPVPTSHELTQAE-GYPAEYIMTSSDHQVSGKTYITNSKREKLPNVS  195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      147 ITDPEI---PPSNIRRIICSSGSGFPPEHLSMLENGE-LNAIDITYVSQPELEYTVSS  202
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy      196 TLRINTTNNELFYC-----TERRLDPEENHTAEVLIDELPLAPPNERTHLVIL  244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      203 KLDFEMTNTNHSFYLICRYGHLRVNQTFENMNTPKOEHPHMDLPSMAT-----TLISVN  255
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy      245 GAILICLGVALTFLF--RLRGR  265
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      256 GIFYIC--CLTYCFAPRCRRR  275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 7

I46690

CD80 precursor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999

C:Accession: I46690

R:Isomono, T.: Seto, A.

Immunogenetics 42, 217-220, 1995

A:Title: Cloning and sequencing of the rabbit gene encoding a cell costimulatory mole

A:Reference number: I46689; MUID:95369849

A:Accession: I46690

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-299 <I70>

A:Cross-references: GB:DA9843; NID:g755096; PIDB:BAA08643.1; PID:g755097

C:Superfamily: B-Lymphocyte restricted antigen B7

Query Match	10.7%	Score	162	DB	2	length	299
Best Local Similarity	19.6%	Pred	No. 2e-05				
Matches	52	Conservative	59	Mismatches	100	Indels	54
						Gaps	12

QY	25	KDLVVEKSGMMTECKFPVEKODLALLIYVMEDEKXNIIGFVHGEDLKVOHSSYROR	84
Db	42	KEMALSCDYIISID-----ELKMRITWOKDOOMVLSITISGVEWPEPKR----	88
QY	85	ARLLKDOLSICNALQITVYKLODAGVYRCMISYG-GADYKR-----IYVYAPAYNK	136
Db	89	RTEPFD--INNLSIMLIALSLDKGYTCVQKNGENSGFRREILTSVFLSI RADPVPSS	145
QY	137	INORLIYVDPYTSHEHLTCQAE-GYRAEYIWMSSDHQVLSGTTTTNSKREKRLPNVYS	195
Db	146	ITD---:IGHPPNWKRIJCSGSGGFPPRIAM-MEDEBELAAVNTVDDIDJLETYSVS	201
QY	196	TLRINTTNEIEYCFTRLRDPBEENHTAEIYIPEL-----PLAHPENBRT-----H	240
Db	202	ELDFNVNTNHSIYCLIK-----YGLSISOIFPMPSKRKQEPIDQLPFWTIPVSGA	253
QY	241	LVIILGAILLCLGVALTFTIFRLAKKR	265
Db	254	LVLTAIVAVLYCL--ACRHVAARKKTR	276

RESULT 8
A48754 B7-2 antigen - human
N.Alternate names: B7.0 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
C.Species: Homo sapiens (man)
C.Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999
R.Accession: A48754; S39055
R.Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restifo Jr., V.A.; Lombard

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 06:35:58 ; Search time 25.77 Seconds

(without alignments)
412.604 Million cell updates/sec

Title: US-09-649-108-1

Sequence: 1 MRFAVFIMTYHLLNFT.....KCGIDPTNSKSDTHLEET 290

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 100059 seqs, 3664827 residues

number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	210	13.9	524	1	BUTY_MOUSE
2	174	11.5	526	1	BUTY_BOVIN
3	172	11.4	288	1	CD80_HUMAN
4	169.5	11.2	306	1	CD80_MOUSE
5	169	11.2	526	1	BUTY_HUMAN
6	165	10.9	322	1	ICOL_MOUSE
7	162	10.7	299	1	CD80_RABIT
8	161.5	10.7	329	1	CD86_HUMAN
9	161	10.7	330	1	CD86_RABIT
10	153.5	10.2	302	1	ICOL_HUMAN
11	139.5	9.2	319	1	A33_HUMAN
12	137	9.1	365	1	CXAR_HUMAN
13	134.5	8.9	298	1	VEJA_HUMAN
14	132	8.7	853	1	NCAL_BOVIN
15	130	8.6	1088	1	NCAL_XENLA
16	128	8.5	1092	1	NCAL_XENLA
17	127.5	8.4	309	1	CD86_MOUSE
18	126	8.3	1106	1	PCDR_HUMAN
19	122	8.1	321	1	TCB_FLV
20	122	8.1	761	1	NCAL_HUMAN
21	122	8.1	848	1	NCAL_HUMAN
22	121.5	8.0	1338	1	VGRI_HUMAN
23	120.5	8.0	646	1	MU18_HUMAN
24	120	7.9	365	1	CXAR_MOUSE
25	119.5	7.9	345	1	LACH_SCHAM
26	119.5	7.9	2333	1	PCGA_CANFA
27	118.5	7.8	588	1	C166_CHICK
28	118	7.8	725	1	NCAL_MOUSE
29	118	7.8	1115	1	NCAL_MOUSE
30	117.5	7.8	359	1	LACH_DROME
31	117.5	7.8	2132	1	PCGA_MOUSE
32	115.5	7.6	333	1	AMAL_DROME
33	115	7.6	299	1	JAM1_HUMAN

34	115	7.6	1091	1	NCAL_CHICK	p1590 gallus galli
35	115	7.6	1336	1	VGRI_RAT	p53767 rattus norv
36	114.5	7.6	2415	1	PCGA_HUMAN	p13112 homo sapien
37	114	7.5	588	1	NCAL_RAT	p13596 rattus norv
38	111	7.3	583	1	C166_HUMAN	Q1740 homo sapien
39	111	7.3	583	1	C166_MOUSE	O6190 mus musculu
40	110.5	7.3	2124	1	PCGA_RAT	p07897 rattus norv
41	110.5	7.3	2364	1	PCGA_BOVIN	p13608 bos taurus
42	110	7.3	626	1	MAG_RAT	p07722 rattus norv
43	109.5	7.2	274	1	OX2G_HUMAN	p41217 homo sapien
44	109	7.2	626	1	MAG_HUMAN	p20916 homo sapien
45	109	7.2	1443	1	NEOL_CHICK	O90610 gallus galli

ALIGNMENTS

RESULT 1
BUTY_MOUSE STANDARD: PRT: 524 AA.
AC Q62556: P97392;
BT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
GN BTN1A1 OR BTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN-129; TISSUE-Mammary gland;
RC MEDLINE-97148936; PubMed-8995761;
RA Ogg S. L., Komaragiri M. V. S., Mather I. H.;
RT "Structural organization and mammary-specific expression of the
RT butyrophilin gene".
RL Mamm. Genome 7:900-905(1996).
RN [2]
RP SEQUENCE OF 39-487 FROM N. A.
RC TISSUE-Mammary gland;
RC MEDLINE-96125722; PubMed-8541302;
RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura K., Matsuda T.;
RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin
RT specifically associates with a 150-kDa protein of mammary epithelial
RT cells and milk fat globule membrane".
RL Biochim. Biophys. Acta 1245:285-292(1995).
CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
CC -!- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
CC PREGNANCY AND IS MAXIMAL DURING LACTATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 1
CC V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PH-PROTEIN (RFP).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: U67065; AAB51034.1; -;
DR EMBL: S80642; AAB35893.1; -;
DR MGD: MGI:103118; Btn1a1.
DR InterPro: IPR003879; Butyroph_DUF_C.

Db 15 IFILLQPKLDSAPFDYIGQEPILLAVGEDALPCR--LSPNVSAKGMELRFRKVP 72
 Oy IOEV--HGEEDLKQVHSSRYORARLLKDLQSLGNAALQITVVKLQDAGVRCMISYGCAD 122
 Db 73 AVFYSRRCQDEQGEEMAEKRVSLVEDHIAEGSVAVRIQVKAASDCEYCFRQ--DEN 131
 Oy 123 YKRTIVKVAAPYKINORILLVDPVTSHELTCQAE--YPKAEVITWSSDHQVLSGKTTT 181
 Db 132 YEELVHLKVAALGSDPHISMVKVQESGEIOLECTSVGWYPERQVWRTHREEPSMS 191
 Oy 182 TNSREKRLNVSTLANTNTNEIFCTFRRLDPEENHTALVPELPLAHPNERHIL 241
 Db 192 RNDP--EGELFTVRAVIRRSKMNVCCTIRNLLGQEKVEV---SLPASFPLTPPM 247
 Oy 242 VIICAILLCIGV---ALTFIFRLKRCMMDVKKGIQDTNKKQSDPHIE 289
 Db 248 VAVAVILVIGLITIGSIFFTWRILYKERSR-----QRNRFSSKELLEE 292
 RE T 3
 C HUMAN STANDARD: PRT: 288 AA.
 I CD80, HUMAN
 AC P33681;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1
 DE ANTIGEN (CTLA-4 COUNTER-RECEPTOR B7.1) (B7) (BBI).
 CN CD80 OR CD28LG1 OR CD28LG OR LAB7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lymphoid.
 RX MEDLINE=90010147; PubMed=2794510;
 RA Freeman G.J., Freedman A.S., Segall J.M., Lee G., Whitman J.F.,
 RA Nadler L.M.;
 RT "87, a new member of the Ig superfamily with unique expression on
 RT activated and neoplastic B cells.";
 RL J. Immunol. 143:2714-2722(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92307753; PubMed=1377173;
 RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
 RA Dupont B.;
 RT "Genomic organization and chromosomal location of the human gene
 RT encoding the B-lymphocyte activation antigen B7.";
 RL Immunogenetics 36:175-181(1992).
 RN [3]
 RP SEQUENCE OF 35-38.
 RX MEDLINE=91341422; PubMed=1714935;
 RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
 RA White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
 RT "Structure, expression, and T cell costimulatory activity of the
 RT murine homologue of the human B lymphocyte activation antigen B7.";
 RL J. Exp. Med. 174:625-631(1991).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
 CC AND DENDRITIC CELLS.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -1- DATABASE: NAME=PROV: NOTE=CD guide CD80 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd80.htm".
 CC -----
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 CC or send an email to license@isb.slb.ch).
 CC -----
 DR EMBL: M27533; AAA56045.1; -
 DR EMBL: M83077; AAA58390.1; -
 DR EMBL: M83072; AAA58390.1; JOINED.
 DR EMBL: M83073; AAA58390.1; JOINED.
 DR EMBL: M83074; AAA58390.1; JOINED.
 DR PIR: A45803; A45803.
 DR MIM: 112203; -
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003600; IG_Like.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00410; IG_Like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 34
 FT CHAIN 1 288
 FT DOMAIN 35 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 288
 FT DOMAIN 43 123
 FT DOMAIN 155 223
 FT DISULFID 50 116
 FT DISULFID 162 216
 FT CARBOHYD 53 53
 FT CARBOHYD 89 98
 FT CARBOHYD 98 98
 FT CARBOHYD 186 186
 FT CARBOHYD 207 207
 FT CARBOHYD 211 211
 FT CARBOHYD 226 226
 FT CARBOHYD 232 232
 SQ SEQUENCE 288 AA; 33048 MW; BA453EE34528B1F4 CRC64;
 Query Match 11.4%; Score 172; DB 1; Length 288;
 Best Local Similarity 22.1%; Pred. No. 8.7e-08;
 Matches 58; Conservative 56; Mismatches 97; Indels 52; Gaps 12;
 Oy 25 KDLYVEYSGNMWTECKRPFVEKQDLALIVWEEDNIIQFVGEDDKAKQHSYROR 84
 Db 43 KEVATLSGHNVAE-----ELAQTRITWQEKKNVLTAMSGDHNIMPEYKN---- 89
 Oy 85 ARLLKQSLGNAALQITVVKLQDAGVRCMI--SYGADYK-----ITVQVAPYK 136
 Db 90 -RTIFD--ITNNLSVILALRPSDGEYECVYLKTEKAKFKREHLAEVTLASKAFPPPS 146
 Oy 137 INQRLVDPVTSHELTCQAE--GYPKAEVITWSSDHQVLSGKTTIYNSKREKLENVTS 195
 Db 147 ISDEFI--PTSNIRRIICSTSGEPPEHLVLENGEE--LNAINTVVSQDDETELAVSS 202
 Oy 196 TLRIINTTNEIFYC-----TFPRRLDPEENHTALVPELPLAHPNERHIL 244
 Db 203 KLDFMTTNSHSPCLIKYGLRVNQTFFMNTTKQHPDNLIPSWAI-----TLISVN 255
 Oy 245 GAILLCGLVATLTFP--RLRKGR 265
 Db 256 GIVFIC---CLTYCAPRCRRR 275

RESULT	4			
ID	CD80_MOUSE	STANDARD:	PRT:	306 AA.
AC	000609.			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1 ANTIGEN) (B7).			
GN	CD80 OR B7.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=91341422; PubMed=17114935;			
RA	Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,			
RA	White M., Fingerhuth J.D., Grubben J.G., Nader L.M.;			
RA	Structure, expression, and T cell costimulatory activity of the			
RL	murine homologue of the human B lymphocyte activation antigen B7.;			
RL	J. Exp. Med. 174:625-631(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=93307789; PubMed=7686531;			
RA	Selvakumar A., White P.C., Dupont B.;			
RA	Genomic organization of the mouse B-lymphocyte activation antigen			
RT	B7.;			
RL	Immunogenetics 38:292-295(1993).			
CC	-1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T			
CC	LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE			
CC	PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS			
CC	RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA			
CC	INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL			
CC	MALIGNANCIES.			
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-			
CC	ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND			
CC	IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.			
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS			
CC	ONE C2-LIKE AND ONE V-LIKE DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X60958; CAA43291.1; -			
DR	EMBL; L12589; AAA37240.1; ALT_SEQ.			
DR	EMBL; L12585; AAA37240.1; JOINED.			
DR	EMBL; L12586; AAA37240.1; JOINED.			
DR	EMBL; L12587; AAA37240.1; JOINED.			
DR	EMBL; L12588; AAA37240.1; JOINED.			
DR	PIR; S17291; S17291.			
DR	MGI; MGI:101775; Gdb0.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003600; IG_1like.			
DR	Pfam; PF00047; Ig_2.			
DR	SMART; SM00409; Ig_1.			
DR	SMART; SM00410; IG_1like; 1.			
RV	Immunoglobulin domain; T-cell; glycoprotein; signal; Transmembrane;			
RV	Receptor.			
FT	SIGNAL	1	37	
FT	CHAIN	38	306	T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT	DOMAIN	38	246	INTRACELLULAR (POTENTIAL).
FT	TRANSMEM	247	268	POTENTIAL.

[illegible]

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U39576; AAC50489.1; -
DR MIM: 601610; -
DR InterPro: IPR003879; Butyrophil_DUF_C.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR InterPro: IPR003877; SPRY.
DR Pfam: PF00047; 19; 1.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00449; SPRY; 1.
DR Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
KM SIGNAL 1 26
FT CHAIN 27 526
FT DOMAIN 27 526 BUTYROPHILIN.
FT TRANSMEM 243 269 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 270 526 POTENTIAL.
FT CARBOHYD 55 55 CYTOPLASMIC (POTENTIAL).
F CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 526 AA; 59004 MW; E9ECA0CF8DAF94D5 CRC64;

Query Match 11.2%; Score 169; DB 1; Length 526;
Best Local Similarity 25.2%; Pred. No. 3.6e-07;
Matches 64; Conservative 44; Mismatches 132; Indels 14; Gaps 7;

DY 19 FTVTPKDLVVEYGSNMTIECKPEVEKQDLALIVYWEKDKNIQFVH--GREDLKV 76
DY 29 FDVIGPPEPIALVAVGDEALPCR--LSPNASAEHLELRFMKKVPALVHRDGEQAE 86
DY 77 QHSYRQARALLKQLSIGNALQITDYKLODAGYRCMISYGCADYRITYKVAAPLNK 136
DY 87 QMPYRGKATLVQDGIAGVALRIGVRSDDGEYTCFFREDGS-YEALVHLKVAALG 145
DY 137 INORILVNDPTSEHLELCOAEG-YPKAEVMTSSDHQVLSGKTTTTSKREKLFNTS 195
DY 146 SDPHISMVQNGECLLECTSVGWTPPEQOVQWRTSKGKFP-STSEKNNPDEEGIFTYAA 204
DY 196 TLRINTTNEIFYCTFRRLDEENHTALVPELPAPNPERHVLVILGLCLGV-- 253
DY 205 SVIIRDSTKNVSCYIQLLIGQEKVEISIPASL--PLTLPVAVAVAVILWGLLT 261
DY 254 --ALTFIFRLAKGR 265
DY 262 IGSIFFTWRLYNER 275
RESULT 6
ICOL_MOUSE STANDARD: PRT: 322 AA.
AC G9JHUB;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ICOS LIGAND PRECURSOR (B7 HOMOLOG 2) (B7-H2) (B7-LIKE PROTEIN GL50)
DE (B7-RELATED PROTEIN-1) (B7RP-1) (LICOS).
GN ICOSL OR B7H2 OR B7RP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Lymphocytes;
RX PubMed=10617205;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A.,
RA Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
RA Elliott G.S., Hui A., McCabe S.M., Scully S., Shalinian A.,
RA Shaklee C.L., Van G., Mak T.W., Senaldi G.,

RT "T-cell co-stimulation through B7RP-1 and ICOS".
RL Nature 400:827-832(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thymus;
RX PubMed=10549624;
RA Swallow M.M., Wallin J.J., Sha M.C.;
RT "B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by
RT TNFalpha.";
RL Immunity 11:423-432(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C3H/HeJ; TISSUE=fetal thymus;
RX MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
RA Jacobs K.A., Collins M.;
RT "Identification of GL50, a novel B7-like protein that functionally
RT binds to ICOS receptor.";
RL J. Immunol. 164:1653-1657(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=peripheral blood lymphocytes;
RX MEDLINE=21286479; PubMed=11390480;
RA Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.,
RA Collins M.;
RT "Differential expression of inducible costimulator-1ligand splice
RT variants: lymphoid regulation of mouse g150-b and human g150
RT molecules.";
RL J. Immunol. 166:7300-7308(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Ling V., Dunnst-Joannopoulos K.;
RT "g150 molecules and uses thereof.";
RL Patent number WO0121796, 29-MAR-2001.
CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
CC TH2 PHENOTYPE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: 1 (SHOWN HERE) AND 2/B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
CC (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S
CC PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
CC CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
CC -1- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYONISTS; IN THE YOLK
CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
CC 14.5 DPC.
CC -1- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC EMBL: AF216747; AAF45149.1; -

DR EMBL: AF199027; AAF34738.1; -
 DR EMBL: AX100591; CAC36463.1; -
 DR EMBL: AX100593; CAC36464.1; -
 DR EMBL: AF394451; AAK77544.1; -
 DR MGI:1354701; Icos1.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; Ig_1.
 DR SMART: SM00410; Ig_Like; 1.
 DR B-cell activation; Immune response; Glycoprotein;
 KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 KW Alternative splicing.
 FT SIGNAL 1 46
 FT CHAIN 1 322
 FT DOMAIN 47 277
 FT TRANSMEM 278 298
 FT DOMAIN 299 322
 FT DOMAIN 55 145
 FT DOMAIN 178 250
 FT DOMAIN 31 38
 FT DOMAIN 289 292
 FT DISULFID 62 138
 FT DISULFID 185 243
 FT CARBOHYD 71 71
 FT CARBOHYD 120 120
 FT CARBOHYD 163 163
 FT CARBOHYD 200 200
 FT CARBOHYD 213 213
 FT CARBOHYD 252 252
 FT CARBOHYD 265 265
 FT VARSPLIC 321 322
 FT CONFLICT 237 237
 FT SEQUENCE 322 AA; 35960 MW; 55CCBAAD12E47B6 CRC64;
 Query Match 10.9%; Score 165; DB 1; Length 322;
 Best local Similarity 23.8%; Pred. No. 4.1e-07;
 Matches 56; Conservative 37; Mismatches 100; Indels 42; Gaps 8;
 QY 33 GSNMTECKRPVEKQDLALIVYWEDEKNI--IOFVGEEDLKVOHSSYRORALK 89
 DB 55 GSNVLSCLDIPHRHNFSLSLYVWQIENPEVSATYVLPKSPGINDV--SSYKRGHLSL 113
 QY 90 DQSLGNAALQITDVKLDODAGYRCMISYGADYKRTVYNAPYKINORILVDPVTS 149
 DB 114 DSKKQGNFSLYKLVNTPQDQOFTGRVFMNATE--LVKILEEYVLRVAANSTFVIS 170
 QY 150 -----EHELTCQAE-GYPAEVIWTSDDQVLSGKTTTNSKREEK--LEFNTSTL 197
 DB 171 TSDSNPGORERTYCMKSNKNGYEPENLVWINTDNLIDFALQNTVTYLNKLGIDYDVLST 230
 QY 198 RINTTNEIFYCTFRRL-----DPEENTALL--VIPLEL 229
 DB 231 RLPMTSKGVLLCCVENVALHONITSSIOAESFTGNNKNTKQOETHNELKVLVPLV 285
 RESULT 7
 CD80_RABIT STANDARD; PRT; 299 AA.
 AC P42070;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1
 DE ANTIGEN).
 GN CD80.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B/J X CHBB:HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules."
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC *****
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: D49843; BAA08643.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; Ig_1.
 DR SMART: SM00410; Ig_Like; 1.
 DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 32
 FT CHAIN 33 299
 FT DOMAIN 33 243
 FT TRANSMEM 244 264
 FT DOMAIN 265 299
 FT DOMAIN 42 122
 FT DOMAIN 154 222
 FT DISULFID 49 115
 FT DISULFID 161 215
 FT CARBOHYD 52 52
 FT CARBOHYD 88 88
 FT CARBOHYD 97 97
 FT CARBOHYD 122 122
 FT CARBOHYD 185 185
 FT CARBOHYD 206 206
 FT CARBOHYD 210 210
 FT SEQUENCE 299 AA; 33513 MW; 67442235E5CC91DE0 CRC64;
 Query Match 10.7%; Score 162; DB 1; Length 299;
 Best local Similarity 19.6%; Pred. No. 6.8e-07;
 Matches 52; Conservative 59; Mismatches 100; Indels 54; Gaps 12;
 QY 25 KDLYVEGSGNMTECKRPVEKQDLALIVYWEDEKNIIOFVGEEDLKVOHSSYROR 84
 DB 42 KEMALSCDYNISID-----ELARMRYMOKDOOVMYLSISGQVEMPEKKN----- 88
 QY 85 ARLLKQDLSGNALQITDVKLDODAGYRCMISYG-ADYKR-----ITVYNAPYK 136
 DB 89 -RTPPD--IINNSLMLTALRLSDKGYTTCVOKENGESFRREHLTVSTLSIRADFPVPS 145
 QY 137 INCRILVDPVTSHELTCQAE-GYPAEVIWTSDDQVLSGKTTTNSKREEKLVNPTS 195
 DB 146 ITD---IGHDPNPKRIRCSASGSGFPEPRILAW-MEDEBELNAVVTYDQDLPTFLYSVSS 201
 QY 196 TLRINTTNEIFYCTFRRLDPEENHTALVIPLEL-----PLAMPNERT-----H 240
 DB 202 ELDFNVTNNHSIYCLIK-----YGLSVSQIFPMSKPKQEPPIQLPLHWIIPVSGA 253
 QY 241 LVILGAILLCLGVALTFIFRLRGR 265

ID CD86_RABIT STANDARD: PRT: 330 AA.
AC P42071;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 DE ANTIGEN).
GN CD86.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/J X CHBB:HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules."
RT Immunogenetics 42:217-220(1995).
CC 1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY BINDING CD28 OR CTLA-4, MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC 2- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC 3- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL: DA9842; BAA08642.1; -
CC InterPro: IPR003006; IG_MHC.
CC DR InterPro: IPR003596; IG_v.
CC SMART: SM00406; IG: 1
CC DR PROSITE: PS00290; IG_MHC: 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGINL 1 22 POTENTIAL.
FT CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 23 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 330 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 149 225 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 157 218 POTENTIAL.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 330 AA: 37142 MW: 9350DD65C57E3EB1 CRC64;

Query Match 10.7% Score 161. DB 1: Length 330;
Best Local Similarity 23.3% Pred. No. 9.5e-07;
Matches 67; Conservative 52; Mismatches 117; Indels 52; Gaps 12;

OY 32 YGSMTPECKFPYERKODLAALIYVEMEDKNIT-QFVHGEBDKVOHSSYRQARLLKD 90
DB 32 FNTADLPQCFPTNSQSHSLSELYVFWODERLYLYELFLGRE--KPDVNDPKYIGRTSFD 89

OY 91 QLSGNALQITDYKLODAGVYRCMISYGADYKRTFVKVNPYKINORTI.VVDPVT-- 148
AC 075144; Q9NR01; Q9HD18; PRT: 302 AA.
DT 15-JUL-1999 (Rel. 38, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ICOS LIGAND PRECURSOR (B7 HOMOLOG 2) (B7-H2) (B7-LIKE PROTEIN GL50) (B7-RELATED PROTEIN-1) (B7RP-1).
GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Dendritic cell;
RX PubMed11023515;
RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds ICOS."
RT Blood 96:2808-2813(2000).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Peripheral blood lymphocytes;
RX PubMed11007762;
RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K., Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H., Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
RT "Characterization of a new human B7-related protein: B7RP-1 is the ligand to the co-stimulatory protein ICOS."
RT Int. Immunol. 12:1439-1447(2000).
RL [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocytes;
RX MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Flimerty H.F., Bean K.M., Spaulding V., Fouser L.A., Leonard J.P., Hunter S.E., Zolnier R., Thomas J.L., Miyashiro J.S., Jacobs K.A., Collins M.;
RT "Identification of GL50, a novel B7-1-like protein that functionally binds to ICOS receptor."
RL J. Immunol. 164:1653-1657(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."
RL DNA Res. 5:169-176(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Ling V., Dunnusi-Joannopoulos K.;
RT "GL50 molecule and uses therefor."

OY 242 VILGATILGVALTFIFRLKGRMDYKKGIDJTSKQSDTHLE 289
DB 252 VALTLIVCGIVLFTLMKRKKEQDPVCEC--ETIKDKAKENHVEE 297

DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG-like; 1.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319
FT DOMAIN 22 235
FT TRANSMEM 236 256
FT DOMAIN 257 319
FT DOMAIN 36 124
FT DOMAIN 139 229
FT DOMAIN 258 261
FT DISULFID 43 117
FT DISULFID 162 211
FT DISULFID 146 222
FT CARBOHYD 112 112
FT CARBOHYD 200 200
FT CARBOHYD 223 223
SC SEQUENCE 319 AA; 35632 MW; 9BFC7A9F45C2408E CRC64;
Query Match 9.28; Score 139.5; DB 1; Length 319;
Best Local Similarity 22.08; Pred. No. 6,7e-05;
Matches 58; Conservative 47; Mismatches 106; Indels 53; Gaps 11;
DB 16 LNATVTPVDLYVEYSGNMTECKFPVEK-----QDLAL-----IVYEMEDKN 63
19 VDAISVETPDVLAASGSKSTLPCTYHTSTSSREGLIOMDKLLITERVYIPFSKN 78
QY 64 IIOFVEEDLKVQHSYRORARLLKDLSGN-----ALQITDVKLQADAGYRCMIS 117
DB 79 ---YIHE-----LYKNRVSISNNAEQSDASITIDQLTMADNGYECVS 120
QY 118 -----YGGADVKRTIVKYNAPINKINORLVDPYTSHELTQQA-EGYKAEVITWSDH 172
DB 121 LMSDLENTKSRVALLVLPSPKCEGIEGTIGNNQLQCSKESPPQYSW--KRY 178
QY 173 QVLSGKTTTNSKREKLEFNTSTLRINTTNEIFCYGFRLDPEE--NHTAEVILPELP 230
DB 179 NILNDEPPLAOPASGOV-----SLKNISTDTSGYICTSSNEGTORCINITVAVRPSMN 234
QY 231 LA---HPNERTHLVILGAILLC 250
DB 235 VALYVGIAVGVALIITIGIITTC 258
R 12
CXAR_HUMAN STANDARD; PRT; 365 AA.
ID P78310; 000694;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR PRECURSOR (COXSACKIEVIRUS B-
ADENOVIRUS RECEPTOR) (HCAR) (CVB3 BINDING PROTEIN).
GN CXADR OR CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97191019; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Kitchin A., Hong J.S., Horvitz M.S., Crowell R.L., Finberg R.W.,
RT Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5.
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.

RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20008750; PubMed=10543405;
RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
RT "Genomic organization and chromosomal localization of the human
RT coxsackievirus B-adenovirus receptor gene";
RL Hum. Genet. 105:334-339(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Anderson C.W., Kleczkawa J., Dunn J.J., Fretwell P.;
RT "Sequence and expression of CXADR, the human gene for the
RT coxsackievirus and adenovirus receptor";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U07593; CA68868.1; -;
DR EMBL: U90716; AAC51234.1; -;
DR EMBL: AF169366; AAF05908.1; -;
DR EMBL: AF169366; AAF05908.1; JOINED.
DR EMBL: AF169361; AAF05908.1; JOINED.
DR EMBL: AF169362; AAF05908.1; JOINED.
DR EMBL: AF169363; AAF05908.1; JOINED.
DR EMBL: AF169364; AAF05908.1; JOINED.
DR EMBL: AF169365; AAF05908.1; JOINED.
DR EMBL: AF200465; AAF24344.1; -;
DR MIM: 602621; -;
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00410; IGV; 1.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT DOMAIN 238 258
FT TRANSMEM 259 365
FT DOMAIN 34 127
FT DOMAIN 135 219
FT DOMAIN 155 219
FT DISULFID 41 120
FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
SC SEQUENCE 365 AA; 40029 MW; AB01C6346CBFB64 CRC64;
Query Match 9.18; Score 137; DB 1; Length 365;
Best Local Similarity 21.58; Pred. No. 0.00013;
Matches 58; Conservative 47; Mismatches 119; Indels 46; Gaps 9;
QY 18 AFTVTPVDLYVEYSGNMTECKFPVEKQDLALIVY-----EMEDKNIIQVYHG 70
DB 19 SLSTTPEEMIEKAKGETAYLPCKFTLSPE-DQGPLDIEMILSPADQKVDQVILLY-SG 76
QY 71 EEDLKVQHSYRORARLLKDLSGNALQITDVKLQADAGYRCMISYGGADYKRTIVKV 130

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Db 77 DKIVDDYDPDLKGRVHFTSNLDKSGDASINVTNLQSLDGTQCAVK-----KA 125
Qy 131 NAFPNKINQRLIYNDP-----VTSEHETCOAGEPKAEVITWSDHOVLGSK 178
Db 126 PGVANRKHILVLYKPSGARCVDGSEIGSDFKICKE---PKGSLPELOYEOKLSDS 181
Qy 179 TTTNRSKREKLEFNTSTLRIINTTNEIFCYFRLDPEENTHAIPELPLAHPNMR 238
Db 182 QKMPSTSLAEHTSSVYSIKNASSEYSGTYCTVRNRVSGSDCLLNLNV-----PPSKK 235
Qy 239 THLVILGAI---LLCLGVALTFIFRLRKR 265
Db 236 AGL-IAGAIIGTLALILGILIFCCRRKR 264

RESULT 13
VEJA_HUMAN STANDARD; PRT; 298 AA.
ID VEJA_HUMAN
P57087;
F 20-AUG-2001 (Rel. 40, Created)
D 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED MOLECULE PRECURSOR (VE-JAM);
GN C21ORF43.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Vascular endothelial cells;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmieri D., van Zante A., Huang C.C., Hammerich S., Rosen S.D.;
RT "Vascular endothelial junction-associated molecule, a novel member of
RT the immunoglobulin superfamily, is localized to intercellular
RT boundaries of endothelial cells."
RL J. Biol. Chem. 275:19139-19145(2000).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
CC SECONDARY LYMPHOID ORGANS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC
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CC
DR EMBL: AF255910; AAF81223.1;
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003600; IG_Like.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00410; IG_Like; 1.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 20
FT CHAIN 21 298
FT
FT DOMAIN 21 238
FT TRANSMEM 239 259
FT DOMAIN 260 298
FT DOMAIN 43 116
FT DOMAIN 148 221
FT DISULFID 50 109
FT
FT POTENTIAL.
FT VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED
FT MOLECULE.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE V-TYPE DOMAIN.
FT IG-LIKE C2-TYPE DOMAIN.
FT POTENTIAL.

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FT DISULFID 155 214
FT CARBOHYD 98 98
FT CARBOHYD 187 187
FT CARBOHYD 236 236
SQ SEQUENCE 298 AA; 33207 MW; CA7B518E22DCAEE CRC64;
POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Query Match 8.9%; Score 134.5; DB 1; Length 298;
Best Local Similarity 21.4%; Pred. No. 0.00017;
Matches 65; Conservative 52; Mismatches 112; Indels 75; Gaps 16;
Qy 18 AFTVVPKDLVY---VEGSSNMTIECKFP---VEKOLDLAALIVYEMEDKNILQFVHGE 71
Db 26 AYGFSAKPKQOQVTVAVEY-QEALIACTPKTKTVSSRL-----WKRIGRS-VSPVYVO 76
Qy 72 EDLKVQHSRROPARILKQDLSGNALDITPVKLDQADGVYRCMI SYGADYKRITVKYN 131
Db 77 QTLQ---GDFKNRAEMI-----DFNIRIKVTRSDACKYRCIWSAPSEOGQ-----N 120
Qy 132 APYKNINQRLIYNDPVTSEH-----ELTQO-AGEYKAEVIWNSDHOVLGSKT 179
Db 121 LEEDVTLEVLVAPAPVSCPEPSSALSGTVVELRCODKCGNPAPEYTWKKGDIRLENPR 180
Qy 180 TTTNRSKREKLEFNV-TSTLRINTTT-----NEIFY--CIFRLDPEENTHAIEL 224
Db 181 LGSQSTNSSTYMTKTGTGLFMTVSKLDGEGYSCEARNSVGKRCGKRMQDDILNISGI 240
Qy 225 VIPELPLAHPNERHLVILGAILLCLGVALTFIFRLRGRMIDYKKGCIQDTNSKQSD 284
Db 241 I-----AAVVVALVIVSGLGIV--CYAQRKGYES--KETSFOKSSNSSSKAT 283
Qy 285 THLE 288
Db 284 TMSF 287

RESULT 14
NCAL_BOVIN STANDARD; PRT; 853 AA.
ID NCAL_BOVIN
P31836;
F 01-JUL-1993 (Rel. 26, Created)
D 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURAL CELL ADHESION MOLECULE, 140 KDA ISOFORM PRECURSOR (N-CAM 140)
DE (NCAM-140).
GN NCAM1 OR NCAM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain cortex;
RX MEDLINE=89378239; PubMed=2776887;
RA Lipkin V.M., Khramtsov N.V., Andreeva S.G., Moshnyakov M.V.,
RA Petukhova G.V., Rakitina T.V., Feshchenko E.A., Ishchenko K.A.,
RA Mitroeva S.F., Chernova M.N., Drazhysyna S.M.;
RT "Calmodulin-independent bovine brain adenylate cyclase. Amino acid
RT sequence and nucleotide sequence of the corresponding cDNA."
RL FEBS Lett. 254:69-73(1989).
RN [2]
RP SEQUENCE OF 20-36.
RX MEDLINE=86140120; PubMed=3512556;
RA Rougon G., Marshak D.R.;
RT "Structural and immunological characterization of the amino-terminal
RT domain of mammalian neural cell adhesion molecules."
RL J. Biol. Chem. 261:3396-3401(1986).
RN [3]
RP IDENTIFICATION AS N-CAM.
RX MEDLINE=92111748; PubMed=1765159;
RA Premont R.T.;
RT "A bovine brain cDNA purported to encode calmodulin-insensitive

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Query Match	Best Local Similarity	Score 132:	DB 1:	Length 853:
Matches 47:	Conservative 28:	Mismatches 54:	Indels 50:	Gaps 8:
Qy 55	YVWEMEDKNIIIFVIGEDLKVQHSYNGRALLKDDQ--LSIGNAALDITDVKLODAGVY 112			
Db 149	IIMWKGRDVI-----LKKDVRFIYLTNNYLDLRIGIKTKDDEGY 187			
Qy 113	RC--MISGADYKRTIVYKVNAPYNNKINQRLILVVDVPTYSHE--LTCQAEGYKAEVI 166			

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Db      188  PC6GR1IACGEINFDIQIYVNP-PTVQARQSIYNATNLSQSV1LCVNA6GCPHEPIYVS 246
Qy      167  WTSDDHQVLSGRTTTTNSKREKLEINVTSLKINTTNEIFCTERRLDPEENHIAELY 225
Db      247  WKRDGEQI-----ENEDEKYLEFSDSS-----ELTIRKVD--KNDAAEYV 285

RESULT 15
NCAL_XENLA  STANDARD:  PRT:  1088 AA.
AC  P16170:
DT  01-APR-1990 (Rel. 14, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180)
DE  [CONTAINS: N-CAM 140].
GN  NCAM1.
OS  Xenopus laevis (African clawed frog).
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8335;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  MEDLINE-90098671; PubMed-2481269;
RX  Krieg P.A., Sakaguchi D.S., Kintner C.R.;
RT  "Primary structure and developmental expression of a large
RT  cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT  molecule (NCAM).";
RT  Nucleic Acids Res. 17:10321-10335(1989).
CC  -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC  NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC  NEURITES, ETC.
CC  -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC  -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
CC  N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC  -1- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
CC  TISSUE.
CC  -1- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC  TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC  EARLY NEURAL DEVELOPMENT.
CC  -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC  -1- SIMILARITY: CONTAINS 2 FIBRINCTIN TYPE III-LIKE DOMAINS.
CC  -----
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CC  -----
DR  EMBL; M25696; AAA49909.1; -.
DR  PIR; S09600; IJXLNL.
DR  HSSP; P56276; 1TLK.
DR  InterPro; IPR001777; FN_III.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003598; IG_C2.
DR  Pfam; PF00041; I03; 2.
DR  Pfam; PF00047; I9; 5.
DR  SMART; SM00060; FN3; 2.
DR  SMART; SM00408; IGC2; 5.
KW  Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW  Immunoglobulin domain; Alternative splicing; Signal.
FT  SIGNAL 1
FT  CHAIN 20 1088
FT  DOMAIN 20 705
FT  TRANSMEM 706 723
FT  DOMAIN 724 1088
FT  DOMAIN 34 100
FT  DOMAIN 129 193
FT  DOMAIN 225 289
FT  DOMAIN 125 289

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OM protein - protein search, using sw model

Run on: March 18, 2002, 06:35:03 ; Search time 62.55 Seconds
(without alignments)
678.161 Million cell updates/sec

Title: US-09-649-108-1

Perfect score: 1511

Sequence: 1 MRFAVFIFMTWHLNAPT.....KCGIDPTNSKKQSDPHLEET 290

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTRMBL_17:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mhc:*
9: SP_organelle:*
10: SP_phage:*
11: SP_plant:*
12: SP_rodent:*
13: SP_virus:*
14: SP_vertebrate:*
15: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1511	100.0	290	4	09NZ07
2	1050	69.5	290	11	09EP73
3	918	60.8	176	4	09NUZ5
4	404	26.7	273	4	09B051
5	343	22.7	247	11	09W0U5
6	310	20.5	316	4	09BXRI
7	185	12.2	282	4	09H6B2
8	181.5	12.0	296	13	042404
9	181	12.0	329	6	09TRF2
10	179	11.8	288	6	077684
11	175	11.6	288	6	028499
12	174	11.5	296	6	046405
13	170	11.3	286	6	046535
14	169.5	11.2	306	11	09R129
15	167	11.1	526	4	09H458
16	165	10.9	288	6	09BDN6
17	165	10.9	289	6	028347
18	165	10.9	322	11	09HJ8
19	162.5	10.8	272	11	070356

20	162.5	10.8	321	11	055202	092 rattus norv
21	161	10.7	290	11	062680	092680 rattus norv
22	161	10.7	321	11	035187	035187 rattus norv
23	160	10.6	323	6	09BDM9	09BDM9 macaca neme
24	159.5	10.6	326	11	070358	070358 mus musculu
25	159.5	10.6	329	6	09XSX6	09XSX6 felis silve
26	159.5	10.6	332	6	09GCM27	09GCM27 felis silve
27	156	10.3	321	11	062624	062624 rattus norv
28	154.5	10.2	280	6	09TRF1	09TRF1 canis famill
29	153.5	10.2	302	4	09HD18	09HD18 homo sapien
30	153.5	10.2	309	4	09NRQ1	09NRQ1 homo sapien
31	153	10.1	323	6	09BDM4	09BDM4 macaca mula
32	150.5	10.0	323	6	09BDM2	09BDM2 cercopithec
33	150	9.9	323	6	09BDB8	09BDB8 cercocobus
34	148	9.8	292	6	002758	002758 felis silve
35	148	9.8	292	6	09GWM28	09GWM28 felis silve
36	148	9.8	325	6	002838	002838 sus scrofa
37	147.5	9.8	586	4	09HCY2	09HCY2 homo sapien
38	144	9.5	304	6	09TOX1	09TOX1 canis famill
39	144	9.5	523	4	000480	000480 homo sapien
40	143.5	9.5	351	5	09VOY0	09VOY0 drosophila
41	143.5	9.5	527	4	000475	000475 homo sapien
42	143	9.5	325	11	070359	070359 mus musculu
43	140.5	9.3	529	4	P78408	P78408 homo sapien
44	139.5	9.2	284	6	09GL33	09GL33 bos taurus
45	139.5	9.2	319	11	09JKA5	09JKA5 mus musculu

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	290 AA.
09NZ07	09NZ07		
AC	09NZ07		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	B7-H1 (PD-1-LIGAND PRECURSOR).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homi		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20048154; Pubmed=10581077;		
RA	Dong H., Zhu G., Tamada K., Chen L.;		
RT	"B7-H1, a third member of the B7 family, co-stimulates T cell		
RT	proliferation and interleukin-10 secretion.";		
RL	Nat. Med. 5:1365-1369(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PLACENTA;		
RX	Pubmed=11015443;		
RA	Freeman G.J., Long A.J., Iwai Y., Bourque K., Chernova T.,		
RA	Nishimura H., Fitz L., Malenkovich N., Okazaki T., Byrne M.C.,		
RA	Horton H.F., Fouser L., Carter L., Ling V., Bowman M.R., Carreno B.M.,		
RA	Collins M., Wood C.R., Honjo T.;		
RT	"Engagement of the PD-1 immunoinhibitory receptor by a novel B7-family		
RT	member leads to negative regulation of lymphocyte activation.";		
RL	J. Exp. Med. 192:1027-1034(2000).		
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
CC	DOMAIN		
DR	EMBL: AF177937; AAF25807.1; -		
DR	EMBL: AF233516; AAG18508.1; -		
DR	InterPro: IPR003599; Ig		
DR	InterPro: IPR003600; Ig_Like		
DR	InterPro: IPR003006; Ig_MHC		
DR	Pfam: PF00047; Ig_2		
DR	SMART: SM00409; Ig_1		
DR	SMART: SM00410; IG_Like; 1.		
KW	SIGNAL		
FT	SIGNAL	1	18
			POTENTIAL.

FT CHAIN 19 290 PD-1-LIGAND.
SQ SEQUENCE 290 AA: 33275 MM: FE957086E62A31A8 CRC64:

Query Match 100.0%; Score 1511; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 2e-127;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRIFAVFEMTYVHLLNFVTPKDLVYVEYGSNMTECKPPEVKQLDLALIVYWEKE 60
DB 1 MRIFAVFEMTYVHLLNFVTPKDLVYVEYGSNMTECKPPEVKQLDLALIVYWEKE 60
OY 61 DKNITQFVGEEDLKVOHSSYRQRRRLKDLQSLGNALQITDVKLDQAGYRCMTISYGG 120
DB 61 DKNITQFVGEEDLKVOHSSYRQRRRLKDLQSLGNALQITDVKLDQAGYRCMTISYGG 120
OY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
DB 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
OY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
DB 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
OY 181 TTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAHPPNERTH 240
DB 181 TTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAHPPNERTH 240
OY 241 LVITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290
DB 241 LVITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290

RESULT 2

O9EP73 PRELIMINARY; PRT: 290 AA.

AC O9EP73;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PD-1-LIGAND PRECURSOR (B7-H1 PROTEIN).
GN PCDD1L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX PubMed=11015443;
RA Freeman G.J., Long A.J., Iwai Y., Bourque K., Chernova T.,
RA Nishimura H., Filtz L., Malenkovich N., Okazaki T., Byrne M.C.,
RA Horton H.F., Fouser L., Carter L., Ling V., Bowman M.R., Carreno B.M.,
RA Collins M., Wood C.R., Honjo T.,
RT "Engagement of the PD-1 Immunoinhibitory receptor by a novel B7-family
RT member leads to negative regulation of lymphocyte activation.";
RL J. Exp. Med. 192:1027-1034(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Tamura H., Dong H., Zhu G., Sica G.L., Flies D.B., Tamada K., Chen L.;
RT "B7-H1 costimulation preferentially enhances CD28-independent T helper
RT cell function.";
RL Blood 0:0-0(2000).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF233517; AAC18509.1; -;
DR EMBL: AF317088; AAC31810.1; -;
DR MGD: MGI:192646; Pgcd11.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00410; IG_like; 2.
DR Signal.
FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 290 PD-1-LIGAND.
SQ SEQUENCE 290 AA: 32780 MM: AB7C46CF853EBB02 CRC64:
Query Match 69.5%; Score 1050; DB 11; Length 290;
Best Local Similarity 69.4%; Pred. No. 4e-86;
Matches 202; Conservative 34; Mismatches 53; Indels 2; Gaps 2;

OY 1 MRIFAVFEMTYVHLLNFVTPKDLVYVEYGSNMTECKPPEVKQLDLALIVYWEKE 60
DB 1 MRIFAVFEMTYVHLLNFVTPKDLVYVEYGSNMTECKPPEVKQLDLALIVYWEKE 60
OY 61 DKNITQFVGEEDLKVOHSSYRQRRRLKDLQSLGNALQITDVKLDQAGYRCMTISYGG 120
DB 61 DKNITQFVGEEDLKVOHSSYRQRRRLKDLQSLGNALQITDVKLDQAGYRCMTISYGG 120
OY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
DB 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
OY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
DB 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
OY 181 TTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAHPPNERTH 240
DB 181 TTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAHPPNERTH 240
OY 241 LVITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290
DB 241 LVITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290

RESULT 3

O9NU25 PRELIMINARY; PRT: 176 AA.

AC O9NU25;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CDNA FLJ11032 FIS, CLONE PLACE1004197, WEAKLY SIMILAR TO BUTYRPHILIN
DE PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuko Y., Sasaki N.,
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK001894; BAA91966.1; -;
SQ SEQUENCE 176 AA: 19959 MM: E40B76615611F34 CRC64:

Query Match 60.8%; Score 918; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.4e-74;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 115 MISYGADYKRTVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQV 174
DB 1 MISYGADYKRTVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQV 60
OY 175 LSGKTTTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAH 234
DB 175 LSGKTTTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAH 120
OY 61 LSGKTTTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAH 120
DB 61 LSGKTTTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAH 120
OY 235 PNERTHVLITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290
DB 121 PNERTHVLITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 176

RESULT 4

09B051			
ID	09B051	PRELIMINARY:	PRT: 273 AA.
AC	09B051:		
DT	01-JUN-2001 (TREMblrel. 17, Created)		
DT	01-JUN-2001 (TREMblrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMblrel. 17, Last annotation update)		
DE	BTYR0P0PHLIN PRECURSOR B7-DC (PD-1-LIGAND 2 PROTEIN).		
GN	PD1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RA	SEQUENCE FROM N.A.		
RX	MEDLINE=21179366; PubMed=11283156;		
RA	Tseng S.-Y., Otsuji M., Gorski K., Huang X., Slansky J.E., Pal S.I.,		
RA	Shalabi A., Shin T., Pardoll D.M., Tsuchiya H.;		
RT	"B7-DC, a new dendritic cell molecule with potent costimulatory		
RT	properties for T-cells."		
RI	J. Exp. Med. 193:839-846(2001).		
	[2]		
	SEQUENCE FROM N.A.		
RA	Latchman Y., Wood C.R., Chernova T., Chaudhary D., Borde M.,		
RA	Chernova I., Iwai Y., Long A.J., Brown J.A., Nunes R.,		
RA	Greenfield E.A., Bourque K., Bousjotis V.A., Carter L.L.,		
RA	Carreno A.H., Melnickovich N., Nishimura H., Okazaki T., Honjo T.,		
RA	Sharpe A.H., Freeman G.J.;		
RT	"PD-12 is a second ligand for PD-1 and inhibits T cell activation."		
RT	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF329193; AAK31105.1; -		
DR	EMBL; AF344424; AAK15370.1; -		
DR	SEQUENCE 273 AA; 30897 MW; 8B7E963C8BA26EC8 CRC64;		
Q0			

Query Match	26-79%	Score 404	DB 4	Length 273
Best Local Similarity	38.1%	Pred. No. 2.8e-28		
Matches 106	Conservative 40	Mismatches 94	Indels 38	Gaps 10

Q	19	FTVTPKDLVVEYGSNMNTIECKPFVEKOLDLALIVWEMEDKNIIQFVHGSEDLKVOH	78
D <td>21 <td>FTVYVPRKLIIIEHNSNTLECNFPTGSHVNLGALTASIQ-----KVEN <td>64</td> </td></td>	21 <td>FTVYVPRKLIIIEHNSNTLECNFPTGSHVNLGALTASIQ-----KVEN <td>64</td> </td>	FTVYVPRKLIIIEHNSNTLECNFPTGSHVNLGALTASIQ-----KVEN <td>64</td>	64
Q <td>79 <td>--SSYRORARLLDQLSLGNALQITDVKLDAGVYRCMISYGA-DYKRITVKNAPYN <td>135</td> </td></td>	79 <td>--SSYRORARLLDQLSLGNALQITDVKLDAGVYRCMISYGA-DYKRITVKNAPYN <td>135</td> </td>	--SSYRORARLLDQLSLGNALQITDVKLDAGVYRCMISYGA-DYKRITVKNAPYN <td>135</td>	135
D <td>65 <td>DTSPRERATLLEEQLPKGASFHPIQVVRDEGQYCIILYGVAMDYKYLFLKVASYR <td>124</td> </td></td>	65 <td>DTSPRERATLLEEQLPKGASFHPIQVVRDEGQYCIILYGVAMDYKYLFLKVASYR <td>124</td> </td>	DTSPRERATLLEEQLPKGASFHPIQVVRDEGQYCIILYGVAMDYKYLFLKVASYR <td>124</td>	124
Q <td>136 <td>KINRILVVDVYTSHELTQCAEGYPRKAEVMTSSDHOVLGSKTTTTSKREKLEFNYS <td>195</td> </td></td>	136 <td>KINRILVVDVYTSHELTQCAEGYPRKAEVMTSSDHOVLGSKTTTTSKREKLEFNYS <td>195</td> </td>	KINRILVVDVYTSHELTQCAEGYPRKAEVMTSSDHOVLGSKTTTTSKREKLEFNYS <td>195</td>	195
Q <td>125 <td>KINTHILKV-FETDEVELTQATGYPLAEVSPN-----VSPANTSHSRPEGLQVYS <td>178</td> </td></td>	125 <td>KINTHILKV-FETDEVELTQATGYPLAEVSPN-----VSPANTSHSRPEGLQVYS <td>178</td> </td>	KINTHILKV-FETDEVELTQATGYPLAEVSPN-----VSPANTSHSRPEGLQVYS <td>178</td>	178
D <td>196 <td>TLRIITWTNTEIFYCFFRRIDPEENTAEVLPIELPHAPNRITLIVILGAILL--CLGV <td>253</td> </td></td>	196 <td>TLRIITWTNTEIFYCFFRRIDPEENTAEVLPIELPHAPNRITLIVILGAILL--CLGV <td>253</td> </td>	TLRIITWTNTEIFYCFFRRIDPEENTAEVLPIELPHAPNRITLIVILGAILL--CLGV <td>253</td>	253
Q <td>179 <td>VLRLLKPPGRNFSCYF-----WNTIYVRELTLASIDLOSOMERTPTWLLHIFISCT-I <td>232</td> </td></td>	179 <td>VLRLLKPPGRNFSCYF-----WNTIYVRELTLASIDLOSOMERTPTWLLHIFISCT-I <td>232</td> </td>	VLRLLKPPGRNFSCYF-----WNTIYVRELTLASIDLOSOMERTPTWLLHIFISCT-I <td>232</td>	232
Q <td>254 <td>ALTFI---FLRKGRMADYKRCGIGDITNSKOSQSDTHLE <td>288</td> </td></td>	254 <td>ALTFI---FLRKGRMADYKRCGIGDITNSKOSQSDTHLE <td>288</td> </td>	ALTFI---FLRKGRMADYKRCGIGDITNSKOSQSDTHLE <td>288</td>	288
D <td>233 <td>AFIFATVIALRK--QLCOKLYSSKDTTKRPVYTTKRE <td>268</td> </td></td>	233 <td>AFIFATVIALRK--QLCOKLYSSKDTTKRPVYTTKRE <td>268</td> </td>	AFIFATVIALRK--QLCOKLYSSKDTTKRPVYTTKRE <td>268</td>	268

RESULT	5
Q9MWU5	
ID	PRELIMINARY; PRT: 247 AA.
AC	Q9MWU5
DT	01-NOV-1999 (Tremblrel. 12, Created)
DT	01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	BUTYROPHILIN-LIKE PROTEIN.
GN	BTDC.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX	NCBI_TaxID=10090.
NN	[1]

RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Tseng S., Gorski K., Huang X., Pardoll D., Tsuchiya H.;
RT "Butyrophilin like molecule in dendritic cell";
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL; AF142780; AAD33892.1; -;
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART; SM00409; IG_1
DR SMART; SM00410; IG_1like; 1.
SQ SEQUENCE 247 AA; 27819 MW; 9BFDDE14F3EC138F CRC64;

Query Match	22.7%	Score 343:	DB 11:	Length 247:
Best Local Similarity	37.1%	Pred. No. 7, Le-23:		
Matches	92:	Conservative	41:	Mismatches 89: Indels 26: Gaps
OY	19	FTTVPKDLVYVVGSSNMTIECKPFVKOLDIAALIYVWEMEDKNIIGFVHIEEDLKVOH	78	
Db	21	FTTVPKFVYVYDVGVSSVSLCEDDFRRECTELEGI-----RASLQVY--FNFTSLD-	69	
OY	79	SSYRRAELKDKQLSGNALQITVVKLQDDACVYRCMISYGA-DYKRTTVYVNPYNKI	137	
Db	70	---SRALLLEQLPLGRALFHPIPSVQVRRDSQYKCLVIGSANDYKYLTLYVVKASYMKI	126	
OY	138	NORILVDPVTSSEHLETCOAGSYPKAEVYIWTSSDHOVLGSKTTTNSKREELFNVTSTL	197	
Db	127	DTRILEV-PGVGEVOLLTCOARGYPLAEVSW-----QNVSPANTSHIRPECLYQVTSVL	180	
OY	198	RINTTNEIEFTGERLRLPEENHTAEVLVPELPLAHPNERET---FLVILGAILCLGVA	254	
Db	181	RLKPPSRNFSGFMNNAHKELTSA--IIDPLSRNEPKVPKRPVPLHVEIPACTIALIFLA	238	
OY	255	LTFIFRLR 262		
Db	239	IVIIQKR 246		

RESULT	6
09BXRI	
ID	09BXRI
AC	09BXRI;
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	COSTIMULATORY MOLECULE.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxID=9606;
OX	[1]_TaxID=9606;
RP	SEQUENCE FROM N.A.
RX	Pubmed=11224528;
RA	Chapoval A.I., Ni J., Lau J.S., Wilcox R.A., Plios D.B., Liu D.,
RA	Dong H., Sita G.L., Zhu G., Tamada K., Chen L.;
RT	"7-13: A costimulatory molecule for T cell activation and IFN-gamma
RT	production.";
RL	Nat. Immun. 2:269-274 (2001).
DR	EMBL; AF302102; AKK15438.1; -
DR	SEQUENCE 316 AA; 33791 MW; F697007F191CCFA1 CRC64;

	Query Match	Score	DB	Length
20.5%	310	20	316	
Best Local Similarity	30.1%	Pred. No. 8.9e-20		
Matches	85	Conservative	50	Mismatches 133; Indels 14; Gaps 5

[illegible]

RESULT	7
CC	02
AC	09H6B2
AC	09H6B2
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	CNNA: FLJ22418 FIS, CLONE HRC08590.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX	NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RA Kawabata A., Hiki J. T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Ota T., Suzuki Y., Obyashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO IMMUGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AK026071; BAB15349.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00409; Ig_1.
DR SMART: SM00410; Ig_1like; 1.
SQ SEQUENCE 282 AA; 30893 MW; 6F9066999A1E9DB4 C6C64;

Very Match	12.28	Score 185	DB 4	Length 282
Best Local Similarity	23.48	Pred. No. 1.2e-08		
Matches 65	Conservative 55	Mismatches 96	Indels 62	Gaps 15

Db 9 FMSIIIIIIILAGAILIIGIGISGRHSITVTVASAGINCIGEDGIGSCFP--EPDIIKLSD 66

Qy 53 LIIVWEHEDKIIIOFVH---GEEDLQVHSSVYQORARLLKDLQSLGNAALQITDVKLOD 108

Db 67 IVIDMLKE--GVLLIVHEFKGKDELSEODMBEFGRAVPAOVIVGNASRLKKNVOLT 124

Qy 109 AGVYRCMI---SYGADYKRITVKNAPYKINQRIILVDPVTSHEHLTQCA--EGYPKA 163

Db 125 AGTYKCYIITSKGNANLLEKTCFAEPM--EVV----VDYNASSETLCEAPRMPEOP 177

Qy 164 EVIWTSSDHOVLGSKTTTNTNSKREKLEFNTYSLRI-----NTTNTIEPCTFRRLDPEE 218

Db 178 TVVMAS---QVDDQGANSEVSNSTSEELNSEVNTKVVSVLYKNTIINTYSCMI-----E 228

Qy 219 NH----TALVTEPLPLAPPNENETHYLILGA--ILLCL 251

Db 229 NDIAKATGDIKIVTESEI---KRSHSLQLLNNSKASLCV 262

RESULT	ID	AC	PRELIMINARY;	PRT;	296 AA.
042404	042404	042404			
DT	01-JAN-1998	(TREMBLrel, 05, Created)			
DT	01-JAN-1998	(TREMBLrel, 05, Last sequence update)			
DT	01-JUN-2001	(TREMBLrel, 17, Last annotation update)			
DE	CB80-LIKE PROTEIN PRECURSOR.				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Intelestomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RP	[1]				
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RA	O'Regan M.N.;				
RL	Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.				
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.				
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DR	InterPro: IPR003599; Ig.				
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Db 232 SA 233

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GN CD86.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RX MEDLINE=20093996; PubMed=10630300;
LA Yang S., Sim G.-K.;

OM of: US-09-649-108-1 to: GenEmbl:* out_format: pfs
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About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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gb_pat:AX088399	+	1511.00	2633.26	1.7e-138	1553	AX088399 Sequence 3 from Paten
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ACCESSION	AF177937				
VERSION	AF177937.1	GI:6708118			

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SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE	1 (bases 1 to 873)
AUTHORS	Dong, H., Zhu, G., Tamada, K. and Chen, L.
TITLE	B7-H1, a third member of the B7 family, co-stimulates T-cell proliferation and Interleukin-10 secretion
JOURNAL	Nat. Med. 5 (12), 1365-1369 (1999)
MEDLINE	20048154
PUBMED	10581077

REFERENCE	2 (bases 1 to 873)
AUTHORS	Dong, H., Zhu, G., Tamada, K. and Chen, L.
TITLE	Direct Submission
JOURNAL	Submitted (16-AUG-1999) Immunology, Mayo Clinic, 200 First Street, SW, Rochester, MN 55905, USA

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DEFINITION Sequence 3 from Patent WO0114557.
ACCESSION AX088399
VERSION AX088399.1 GI:13397264
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1553)
AUTHORS Wood, C. and Freeman, G. J.

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TITLE Pg 1, a receptor for b7-4, and uses therefor
JOURNAL Patent: WO 0114557-A 3 01-MAR-2001;
DANA-FARBER CANCER INSTITUTE, INC. (US); GENETICS INSTITUTE, INC.
(US)
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ACCESSION AX088422
VERSION AX088422.1 GI:13397287
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1553)
AUTHORS Freeman, G., Boussioutis, V., Chernova, T. and Malenkovich, N.
TITLE Novel b7-4 molecules and uses therefor
JOURNAL Patent: WO 0114556-A 3 01-MAR-2001;
DANA-FARBER CANCER INSTITUTE, INC. (US)
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LOCUS AF233516 1553 bp mRNA PRI 04-OCT-2000
DEFINITION Homo sapiens PD-1-ligand precursor, mRNA, complete cds.
ACCESSION AF233516
VERSION AF233516.1 GI:10567621

KEYWORDS

SOURCE

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1553)

REFERENCE

AUTHORS

Freeman,G.J., Long,A.J., Iwai,Y., Bourque,K., Chernova,T.,
Nishimura,H., Fitz,L.J., Malenkovich,N., Okazaki,T., Byrne,M.C.,
Horton,H.F., Fouser,L., Carter,L., Ling,V., Bowman,M.R.,
Carreno,B.M., Collins,M., Wood,C.R. and Honjo,T.
Engagement of the PD-1 immunoinhibitory receptor by a novel B7
family member leads to negative regulation of lymphocyte activation

J. Exp. Med. 192 (7), 1027-1034 (2000)

JOURNAL

MEDLINE

REFERENCE

AUTHORS

2 (bases 1 to 1553)
Freeman,G.J., Long,A.J., Iwai,Y., Bourque,K., Chernova,T.,
Nishimura,H., Fitz,L., Malenkovich,N., Okazaki,T., Byrne,M.,
Horton,H., Fouser,L., Carter,L., Carreno,B., Collins,M., Wood,C.R.
and Honjo,T.
Direct Submision
Submitted (11-FEB-2000) Adult Oncology, Dana-Farber Cancer
Institute, 44 Binney St., Boston, MA 02115, USA

TITLE

JOURNAL

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ORIGIN

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seq_documentation_block:

LOCUS AX088397 968 bp DNA PAT 17-MAR-2001
DEFINITION Sequence 1 from Patent WO0114557.
ACCESSION AX088397
VERSION AX088397.1 GI:13397262
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 968)
AUTHORS Mood, C. and Freeman, G. J.
TITLE Pd-1, a receptor for b7-4, and uses therefor
JOURNAL Patent: WO 0114556-A 1 01-MAR-2001;
DANA-FARBER CANCER INSTITUTE, INC. (US); GENETICS INSTITUTE, INC.
(US)
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LOCUS AX088420 968 bp DNA PAT 17-MAR-2001
DEFINITION Sequence 1 from Patent WO0114556.
ACCESSION AX088420
VERSION AX088420.1 GI:13397285
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 968)
AUTHORS Freeman, G., Bouslocis, V., Chernova, T. and Malenkovich, N.
TITLE Novel b7-4 molecules and uses therefor
JOURNAL Patent: WO 0114556-A 1 01-MAR-2001;
DANA-FARBER CANCER INSTITUTE, INC. (US)
FEATURES
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BASE COUNT 314 a 209 c 202 g 243 t
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DEFINITION Mus musculus B7-H1 protein mRNA, complete cds.
ACCESSION AF317088
VERSION AF317088.1 GI:11139711
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 873)
Tamura, H., Dong, H., Zhu, G., Sica, G. L., Files, D. B., Tamada, K. and
Chen, L.
B7-H1 costimulation preferentially enhances CD28-independent T
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Blood (2000) In press
2 (bases 1 to 873)
Tamura, H., Dong, H., Zhu, G., Sica, G. L., Ffiles, D. B., Tamada, K. and
Chen, L.
Direct Submission
Submitted (26-OCT-2000) Immunology, Mayo Clinic, 200 First Street,
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    DEFINITION Mus musculus PD-1-ligand precursor, mRNA, complete cds.
    ACCESSION AF233517
    VERSION AF233517.1 GI:10567623
    KEYWORDS
    SOURCE
    ORGANISM
        Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    REFERENCE
        1 (bases 1 to 3593)
        Freeman,G.J., Long,A.J., Iwai,Y., Bourque,K., Chernova,T.,
        Nishimura,H., Fitz,L.J., Malenkovich,N., Okazaki,T., Byrne,M.C.,
        Horton,B.M., Fouser,L., Carter,L., Ling,V., Bowmen,M.R.,
        Carreno,B.M., Collins,M., Wood,C.R. and Honjo,T.
        Engagement of the PD-1 immunoinhibitory receptor by a novel B7
        family member leads to negative regulation of lymphocyte activation
        J Exp. Med. 192 (7), 1027-1034 (2000)
    JOURNAL
        204/72788
    MEDLINE
        2 (bases 1 to 3593)
    REFERENCE
        Freeman,G.J., Long,A.J., Iwai,Y., Bourque,K., Chernova,T.,
        Nishimura,H., Fitz,L., Malenkovich,N., Okazaki,T., Byrne,M.,
        Horton,H., Fouser,L., Carter,L., Carreno,B., Collins,M., Wood,C.R.
        and Honjo,T.
        Direct Submission
        Submitted (11-FEB-2000) Adult Oncology, Dana-Farber Cancer
        Institute, 44 Binney St., Boston, MA 02115, USA
    FEATURES
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            EAEYIWRSDHOPYSGRKSVTTSBEGMLNVTSLKRNATANDVFCTWRSPGON
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17 ATGAGGATATTGTCGCGCATTTATATTCACAGCCCTGCTGCTGCTACG 66
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17 nAlaPheThrValThrValProLysAspLeuTyrValValGluTyrGlys 34
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67 GGCGTTTACTATACAGCGCTCCAAAGACCTGTACGCTGCTGAGTATGGCA 116
34 eArasMetThrIleGluLysLysPheProValGluLysGluLeuLeuAsp 50
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117 GCACGTCACATGAGTGCAGATTCCCTGTAGAACGGGAGCTGACCTG 166
51 AlAlaLeuIleValTyrTrpGluMetGluAspLysAsnIleIleGlnP 67
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
167 CTGCGTTAGTGGTCTACTGGGAAAAGAAATGATGACCAAGTTCACGTT 216
67 eValHisGlyGluGluAspLeuLysValGlnHisSerSerTyrTrpArgL 84
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
217 TGTGGCAGAGAGGAGGAGACCTTAAGCTTCAGACAGCAACTTCAGGGGGA 266
84 rGAlaArgLeuLeuLysAspGlnLeuSerLeuGlyAsnAlaIleLeuGln 100
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
267 GAGCTGCTGCTGCCAAAGACCAAGCTTTTGAAGGCAATGCTGCTTCCAG 316
101 IlleThrasPValLysLeuGlnAspAlaGlyValTyrArgCysMetIleSe 117
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
317 ATCAGACAGCTCAACGCTGACAGACGCGTTTACTGCTGCATTAATCAG 366
117 rTyrGlyGlyAlaAspTyrLysArgIleThrValLysValAsnAlaProt 134
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
367 CTACGCTGTGGGACTACAGCGAATCAAGCTGAAGTCAATGCCCAT 416
134 rYAsnLysIleAsnGlnArgIleLeuValAlaAspProValThrSerGlu 150
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
117 ACCGCAAAATCACACAGAGAAAT...TCCGTGATCCAGCCCTCTGAG 463
151 HisGluLeuThrCysGlnAlaGluGlyTyrProLysAlaGluValIleTr 167
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
464 CATGAACATTAATATGTACAGCGGAGGTTATTCAGAAAGCTGAGGTAAATCG 513
167 pThrSerSerAspHisGlnValLeuSerGlyLysThrThrThrTrpAsn 184
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
514 GACAAACAGTGCACCAACCCGCTAGTGGGAAAGAGATGTCACCACTT 563
184 eLysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
564 CCGGACAGACAGCGCATGCTTCTCATATGACACAGCATGTGAGGTCAAC 613
201 ThrThrThrAsnGluIlePheTyrCysThrPheArgLeuAspProGln 217
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
614 GCCACAGCGCAATGATGTTTCTACTGTACGTTTGGAGATCACACCCAG 663
217 uGlnAsnHisThrAlaGluLeuValIleProGluLeuProLeuAlaHisP 234
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
664 GCAAAACACACAGCGGAGCTGATCATCCCAAGACTGCTGCACACACATC 713
234 rProAsnGluIleArgThrHisLeuValIleLeuGlyAlaIleLeuLys 250
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714 CTCACAGACACAGACGACTCAGTGGGTGCTTCTGGGATCCATCTCTGTTTC 763

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251 LeuGlyValAlaLeuThrPheIlePheArgLeuArgLysGly...ArgMe 266
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764 CTCATTGTAGTGTCCACGCTCCTCTCTTCTTGGACAAAACAGTACAGAT 813
266 tMetAspValLysLysCysGlyIleGlnAspThrAsnSerLysGlns 283
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
814 GCTAGATGTGGGAAATGTGGCTTGAAGATACAGATCAAAACCAACCA 863
283 eArasPThrHisLeuGluGluLysPhe 290
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864 ATGATACACAAATTCAGAGAGAG 886
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seq_documentation_block:
LOCUS AL162253 146327 bp DNA PRI 21-MAR-2001
DEFINITION Human DNA sequence from clone RP11-574F11 on chromosome 9, complete
sequence.
ACCESSION AL162253
VERSION AL162253.17 GI:13677203
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 146327)
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: hinxton@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Apr 19, 2001 this sequence version replaced gi:12539553.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; SW:
SWISSPROT; Tr: TrEMBL; Mp: MOPREP; Information on the MOPREP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormrep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chp9
RP11-574F11 is from the library RP11-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-574F11. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-574F11 is at 146327 in this
sequence. The true left end of clone RP11-635N21 is at 62948 in
this sequence. The true right end of clone RP11-12D24 is at 100 in
this sequence.
FEATURES
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/db_xref="taxon:9606"
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                  /note="Single clone region. Assembly confirmed by
                  restriction digest data."
BASE COUNT      44360 a 29767 c 29483 g 42717 t
ORIGIN

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    Quality: 590.00      Length: 186
    Ratio: 3.960        Gaps: 2
    Percent Similarity: 80.108      Percent Identity: 66.129

alignment_block:
US-09-649-108-1 x AL162253 ..
Align seg 1/1 to: AL162253 from: 1 to: 146327

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34 rAsmetherlleglucylsypheProValGluLysGlnLeuAspLeuA 51
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2716 CAATRTGACAAATGATGCAATATCCAGTAGAAACAAATTAGACCTGG 2765
|||||
51 laAlaLeuIleValTyrTrpGluMetGluAspLysAsnIleIleGlnPhe 67
|||||
2766 CTGCACATAATGTCTATTTGGGAAATGAGAGATAACATTTATTCATTT 2815
|||||
68 ValHisGlyGluGluAspLeuLysValGlnHisSerSerTyrArgGlnAr 84
|||||
2816 GTGCTGTGAGAGAGAACCTGACGCTTACGATCTACACAGACAGAG 2865
|||||
84 gAlaArgLeuLysAspGlnLeuSerLeuGlyAsnAlaIleGlnIle 101
|||||
2866 GGCCGGCTGTGAGAGACACGCTCTCCCTGGAAATGCTGCACCTTCAGA 2915
|||||
101 lerHisPValLysLeuGlnAspAlaGlyValTyrArgCysMetIleSer 117
|||||
2916 TCACAGATGTGAATTCAGATGACAGGGGTGTACCGCTGATGATCAGC 2965
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118 TyrGlyGlyAlaAspTyrLysArgIleThrValLysValAsnAla.... 132
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2966 TATGTGTGCTGCCGACTACAGCGAATTTACTGTGAAGATCAATGTAAGAA 3015
|||||
133 .....ProTyrAsnLysIleA 138
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3016 TTATATATGATGAGAGCCCTGATCTTTATTGAAAACATATTTCCAAAGTGT 3065
|||||
138 sngIleArgIleLeuValValAspProValThrSerGlnHisGluLeuThr 154
|||||
3066 GAAGACTTTTCACTCTGTGAATTCATCTATTTTTCAAACAGAACAGCA 3115
|||||
155 CysGlnAlaGluGlyTyrProLysAlaGluValIleTyrPThr..... 168
|||||
3116 TAGTCTGTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 3165
|||||
169 .....SerSerAspHisGlnValLeuSerGlyLysThrThrThrThr 183
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3166 CAATTTCTTGAGCACCTATTTGATGATGATGATGATGATGATGATGAT 3215
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183 snSerLys 185
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seq_name: gb_pat:AX079673
seq_documentation_block:
LOCUS      AX079673      417 bp      DNA      PAT      22-FEB-2001

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DEFINITION      Sequence 417 from Patent WO0107611.
ACCESSION      AX079673
VERSION      AX079673.1 GI:13159242
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ORGANISM      human.
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS      Baker,K.P., Goddard,A. and Wood,W.I.
TITLE      Human polypeptides and methods for the use thereof.
JOURNAL
PATEENT      WO 0107611-A 417 01-FEB-2001;
                Genentech, Inc. (US)
FEATURES
source
location/Qualifiers
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ORIGIN

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    Ratio: 4.449        Gaps: 5
    Percent Similarity: 91.367      Percent Identity: 87.776

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US-09-649-108-1 x AX079673 ..
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70 LylGluGluAspLeuLysValGlnHisSerSerTyrArgGlnArgAlaA 86
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53 MAGAGGAACACCTGAAAGTTACAGCATANTAGCTACAGACAGANGGCCC 102
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86 rGLeuLeuLysAspGlnLeuSerLeuGlyAsnAlaIleGlnIleThr 107
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103 GGCTGTTNAGGACGACGCTCTCCCTGGNAAATGTGCATTCAGATCAG 152
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103 AspValLysLeuGlnAspAlaGlyValTyrArgCysMetIleSerTyr 118
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153 AGATGTGAATTCAGAGATGACAGGGGTGTACCGCTCATGATCAGCTAT 202
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119 GlyGlyAlaAspTyrLysArgIleThrValLysValAsnAlaProTyrAs 135
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203 GGTGGTCCGCGACTACAGCAATTTNCTGTGAAGATCAATGCCCCCAACA 252
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135 nLysIleAsnGlnArgIleLeuValValAspProValThrSerGlnHisG 152
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253 CAAAAATCAACCAAGAAATTTGTGTGTGATCCAGTCACCTCTGAACAG 302
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152 lLeuLeuThrCysGlnAlaGluGlyTyrProLysAlaGluValIleTyrP 188
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303 AACTGACATGTGAGGCTGAGGTTACCCCAAGGCCAAGTCAATCTGGACA 352
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169 SerSerAspHisGlnValLeuSerGlyLysThrThrThrThrThr 185
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353 AGCAGTGAACATCAATCACTGAGTGTGAAGACACACACCAATTCANA 402
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185 sArgGlu 187
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403 GGCAGAG 409

seq_name: gb_hlg:AC093339
seq_documentation_block:
LOCUS      AC093339      215352 bp      DNA      HNG      20-AUG-2001
DEFINITION      Mus musculus clone RP23-566, WORKING DRAFT SEQUENCE, 10 unordered
                pieces.

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AC093339
 AC093339.1 GI:15213884
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 215352)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Mus musculus, clone RP23-566
 Unpublished
 2 (bases 1 to 215352)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Ferro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hages, B., Heatford, A., Horton, L., Hulme, W., Illey, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Labocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPherson, R., Meldrum, J., Menus, L., Minova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnapp, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (20-AUG-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996, 1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L13374
 Center clone name: 5.G.6
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 211504 bases at least Q40
 Consensus quality: 213314 bases at least Q30
 Consensus quality: 213966 bases at least Q20
 Insert size: 215000; agarose-1p
 Insert size: 214452; sum-of-coverage
 Quality coverage: 10.1 in Q20 bases; sum-of-coverage
 Quality coverage: 10.2 in Q20 bases; sum-of-coverage

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1965: contig of 1965 bp in length
 * 1966 2065: gap of 100 bp
 * 2066 2527: contig of 462 bp in length
 * 2528 2627: gap of 100 bp
 * 2628 4700: contig of 2073 bp in length

4701 4800: gap of 100 bp
 4801 6963: contig of 2163 bp in length
 6964 7063: gap of 100 bp
 7064 10441: contig of 3378 bp in length
 10442 10541: gap of 100 bp
 10542 14119: contig of 3578 bp in length
 14120 14219: gap of 100 bp
 14220 25551: contig of 11332 bp in length
 25552 25651: gap of 100 bp
 25652 61039: contig of 35388 bp in length
 61040 61139: gap of 100 bp
 61140 133497: contig of 72358 bp in length
 133498 133597: gap of 100 bp
 133598 215352: contig of 81755 bp in length.
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 2628. 4700
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 7064. 10441
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 10542. 14119
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 vector_side:right"
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 ORIGIN
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 Percent Similarity: 83.846 Percent Identity: 70.769
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 165672 TCACGGTTACTATCACCGCTCCAAAGACTTGTACGGGTGAGCTATAGG 165623
 33 ySerAsnMetThrIleGluCysLysPheProValGluLysGlnLeuAspL 50
 165622 CAGCAACCTCAGATGAGTGCACATTCCTCGTGAACGAGCACTGCACG 165573
 50 euaAlaAlaLeuIleValTyrTrpGlnMetGluAspLysAsnIleIleGln 66
 165572 TCGTTCGCTTAGTGCTGACGAGAAAGAAATGACCAAGTCAATTCAC 165523
 67 PheValHisGlyGluGluAspLeuLysValGlnHisSerTyrArgGcl 83
 165522 TTGTGTGCAGGAGAGGAGACCTTAAGCTTCAGCAGCAGCACTTCAGCGG 165473

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100  InlethraspyValLysLeuGlnAspAlaGlyValTyrArgCysMetIle 116
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165422 AGATCAGAGAGCTCAAGCTGAGGAGCAGCGGCTTACTGCGTCATTAATC 165373
117  SerTyrGlyGlyAlaAspTyrLysArgIleThrValLysValAsnAla.. 132
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165372 AGCTACGGTGGTGGCGACTACAAGCAATCAAGCAAGTCAATGTTAA 165323
133  ..... ProthrasnLys 136
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165322 GAATTACCTGGATGGGAGAGCTTCATCGATTATTAA 165283
seq_name: gb_pr:AF344424
seq_documentation_block:
AF344424 1223 bp mRNA PRI 02-MAR-2001
LITERATURE Homo sapiens PD-1-ligand 2 protein (PDL2) mRNA, complete cds.
AF344424
AF344424.1 GI:13183882
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1223)
REFERENCE
AUTHORS
Iatchman,Y., Wood,C.R., Chernova,T., Chaudhary,D., Borde,M.,
Chernova,I., Iwai,Y., Long,A.J., Brown,J.A., Nunes,R.,
Greenfield,E.A., Bourque,K., Boussioutis,V.A., Carter,L.L.,
Carreno,B.M., Malenkovich,N., Nishimura,H., Okazaki,T., Honjo,T.,
Sharpe,A.H. and Freeman,G.J.
PD-L2 is a second ligand for PD-1 and inhibits T cell activation
Unpublished
2 (bases 1 to 1223)
TITLE
JOURNAL
REFERENCE
AUTHORS
Iatchman,Y., Wood,C.R., Chernova,T., Chaudhary,D., Borde,M.,
Chernova,I., Iwai,Y., Long,A.J., Brown,J.A., Nunes,R.,
Greenfield,E.A., Bourque,K., Boussioutis,V.A., Carter,L.L.,
Carreno,B.M., Malenkovich,N., Nishimura,H., Okazaki,T., Honjo,T.,
Sharpe,A.H. and Freeman,G.J.
Direct Submission
Submitted (01-FEB-2001) Adult Oncology, Dana-Farber Cancer
Institute, 44 Binney St., Boston, MA 02115, USA
FEATURES
source
1. 1223
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/db_xref="taxon:9606"
/chromosome="9"
/map="p24.2"
1. 1223
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/feature="PDL2"
274..1095
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/db_xref="GI:13183883"
/translation="MIFLLMLSLLEQLQIHALFTVTVKELYIIEGNSVLTLECNF
DTGSHVNLGKATLAKENDTSPHREKATLEKPLGASPIIPVOVYDEGOYOC
IITYGVAMDKYTLIKYKASYRKINPHILKVPEDDELCOAGPYLAESMPNVSIV
PANTSHRTPBGLQVTSVLRKPPGRNRSCTWNTNHYRELTIASIDLOSOMEPRTH
PTWLIHTFTSCIAFTFAIVIALRKQLCKLYSSKDTTKRPVTTTKREVNSAI"
BASE COUNT
ORIGIN
342 a 305 c 257 g 319 t
alignment_scores:
Quality: 411.50 Length: 271
Ratio: 2.286 Gaps: 9
Percent Similarity: 66.421 Percent Identity: 39.114

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alignment_block:
US-09-649-108-1 x AF344424
Align seg 1/1 to: AF344424 from: 1 to: 1223
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334 TTCACAGTACAGTCCCTTAAGCACTGTACATATATAGACATAGGCACCA 384
35 nmetThrIleGlyCysLysPheProValGluLysGlnLeuAspLeuAla 52
||||| ||||||||| ||||||||| ||| |||
384 TGTGACCCCTGGAATGCACTTTGACACTGGAAGTCACTGTGAACCTTGAG 433
52 IalLeuIleValTyrTrpGluMetGluAspLysAsnIleIleGlnPheVal 68
||||| |||
434 CAATAACAGCCAGTTTGCAA..... 453
69 H1SGlyGluGluAspLeuLysValGlnHis.....SerSerTyrArgG1 83
||||| ||||||||| ||| |||
454 .....AAGGTGGAATAATGATACATCCCAACCCAGCTCA 145
83 nargalaargleuleuLysAspGlnLeuSerLeuGlyAsnAlaIalaLeuG 100
||||| ||||||||| ||||||||| ||| |||
486 AAGAGCCACTTGTGCTGGAGGACAGCAGCTGCCCTAGGGAAGCCCTGCTGC 535
100 InlethraspyValLysLeuGlnAspAlaGlyValTyrArgCysMetIle 116
||||| ||||||||| ||||||||| ||| |||
536 ACATATACCTCAAGTCCAAAGTGGAGGACGAAGACAGTACCAATCAATCAATC 585
117 SerTyrGlyGlyAla...AspTyrLysArgIleThrValLysValAsnAl 132
||||| ||| ||| ||| ||| ||| ||| |||
586 ACTATAGGGGTGCGCTGGAGCACTACCAAGTACCTGACCTGAATCAATCAG 635
132 aProTyrAsnLysIleAsnGlnArgIleLeuValYalAspProValYhrS 149
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636 TTCCTACAGAAATAAACAACATCCTCTAAAGGTT...CCAGAAACAG 682
149 ergLHisGlnLeuThrGlyGlnAlaGluGlyTyrProLysAlaGluVal 165
||||| ||||||||| ||||||||| ||| |||
683 ATGAGGTATAGCTCAGCTCCAGGCTACAGGTTATCTCTGGCAGAGTA 7
166 I1etPThrSerSerAspHisGlnValLeuSerGlyLysThrThrThr 182
||||| |||
733 TCCTGGCCCAAC.....GTCAGGCTTCCTGCCACACACAG 767
182 rAsnSerLysArgGluGluLysLeuPheAsnValYhrSerThrLeuArgY 199
||||| ||| ||| ||| ||| ||| |||
768 CCACCTCAGGACCCCTGAAGGCTCTACACAGGTCACACAGTGTCTGCCGC 817
199 IeasThrThrThrAsnGluIlePheTyrCysThrPheArgArgLeuAsp 215
||||| ||| ||| ||| ||| |||
818 TAAAGCCACCCCTGGCAGCAAACTTCAAGCTGTGTGTTTC..... 855
216 ProGluGluAsnHisThrAlaGluLeuValIleProGluLeuProLeuAl 232
||||| ||| ||| ||| ||| ||| |||
856 ...TGGAAATACCTACGTGAGGGAACCTTACTTGGCCAGATTAACCTTCA 902
232 aHisProProAsnGluArgThrHisLeuValIleLeuGlyAlaIleLeuL 249
||||| ||| ||| ||| ||| ||| |||
903 AAGTCAGATGAAACCCAGGACCACTTGGCTTCAATTTTCA 972
249 eu.....CysLeuGlyValAlaLeuThrPheIlePheArgLeuArgLys 263
||||| ||| ||| ||| ||| ||| |||
953 TCCCTCTCTGCATC...ATTGCTTATTTTCAATACCAACAGAGAAACCT 999
264 GlyArgMetMet.AspValLysCysGlyIleGlnAspThrAsnSerLeu 280
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1000 CTAAGAAACAACTCTGTCAAAAGCTGTATCTTCAAAAGACACACAA 1049
280 yslYsgInSer 283
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1050 AAGACCTGTCA 1060

```


OM of: US-09-649-108-1 to: EST:* out-format : pfs

Date: Mar 18, 2002 7:03 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODE=frame+prn.model -DEV=xlh  
-O=Cgnt2_1/USFTO.spool/US09649108/runatc_18032002_063404_19983/app_query.fasta_1.350  
-DB=EST -OFMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500  
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELDEL=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blomsun62 -TRANS=human40.cnt  
-LIST=45 -DOCALLIN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0  
-ALIGN=15 -MAXLEN=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZ=500  
-MINLEN=6 -MAXLEN=2000000000 -USER=US09649108_EGNT_1.3609  
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30  
-NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query: US-09-649-108-1  
Query length: 290  
Database: EST:*  
Database sequences: 11351937  
Search time (sec): 1079221985  
Search time (sec): 1208.980000
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score list:

Sequence	Strd	Orig	ZScore	EScore	Len	Document
gb_est1.AU136409	+	1177.00	2355.97	4.6e-122	784	AU136409 Z550F01.Y5 Soares ovary
gb_est1.AU136409	+	726.00	1451.07	1.2e-71	464	AU136409 Z550F01.Y5 Soares ovary
gb_est1.AU136409	+	713.00	1424.10	3.7e-70	503	AA9292201 Z550F01.Y1 Soares ovary
gb_est1.AU136409	+	618.00	1232.20	1.8e-59	497	BF999743 RC2-GM0136-111100-012-
gb_est1.AU136409	-	565.00	1126.58	1.4e-53	442	AA999416 Z550F01.S1 Soares ovary
gb_est1.AU136409	+	437.50	869.88	2.7e-39	414	AA896104 vx61603.r1 Stratagene
gb_est1.AU136409	+	342.50	679.90	1.7e-28	510	AA821166 vx41606.r1 Soares Mammary
gb_est1.AU136409	+	273.00	531.38	2.0e-20	760	BG574312 602596230F1 NIH_MGC_87
gb_est1.AU136409	+	267.50	519.01	9.6e-20	857	AL537691 AU537691.LT1.FL013.FBT
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gb_est1.AU136409	+	254.50	496.12	1.8e-18	624	AI980757 pat.pK0032.f4.f.chick
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gb_est1.AU136409	+	242.50	469.95	5.2e-17	750	BE367954 601221824F1 NCL.CGAP_1
gb_est1.AU136409	+	208.50	399.70	6.2e-13	1161	BF984597 602309922F1 NIH_MGC_8
gb_est1.AU136409	+	206.00	397.46	5.6e-13	670	AV611199 AV611199.Bos.taurus.1u
gb_est1.AU136409	+	203.00	391.94	1.1e-12	637	AI980097 pat.pK0012.q10 chicken
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gb_est1.AU136409	+	167.00	317.98	1.5e-08	725	B1333927 502999477F1 NIH_MGC_12
gb_est1.AU136409	+	162.50	315.98	1.9e-08	368	BF175563 mp62c06.Y1 Soares.MME
gb_est1.AU136409	+	162.50	312.29	3.1e-08	522	AM632058 91583.MARC.IBOV.Bos.ta
gb_est1.AU136409	+	162.50	308.33	5.2e-08	755	BE916558 601667342F1 NCL.CGAP_1
gb_est1.AU136409	+	159.50	307.66	5.7e-08	456	BE916529 601148267F1 NCL.CGAP_1
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gb_est1.AU136409	+	156.00	301.22	1.3e-07	430	AI455111 mp62c06.X1 Soares.thym
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gb_est1.AU136409	+	152.50	291.80	4.3e-07	537	BF426221 dba23c01.Y1 NICHID.XGC
gb_est1.AU136409	+	151.00	283.79	1.2e-06	860	AL521596 AL521596.LT1.NE1004.NE
gb_est1.AU136409	+	150.50	286.68	8.4e-07	595	BE590174 197160.BARC.5BOV.Bos.b
gb_est1.AU136409	+	148.00	288.06	7.0e-07	324	BE882684 601511150F1 NIH_MGC_71

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gb_est1.AU136409	+	146.50	278.46	2.4e-06	603	AI980757 pat.pK0032.f4.f.chick
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gb_est1.AU136409	+	145.50	278.60	2.4e-06	492	BE509138 db17104.Y1 NICHID.XG
gb_est1.AU136409	+	145.00	276.96	2.9e-06	522	BF454618 u268c11.Y1 NCL.CGAP
gb_est1.AU136409	+	143.50	275.22	3.6e-06	462	AA223133 zt06h05.r1 Stratagene

seq_documentation_block:

LOCUS	AU136409	784 bp	mRNA	EST	24-OCT-2000
DEFINITION	AU136409 PLACE1 Homo sapiens	CDNA clone	PLACE1004197	5'	mRNA
ACCESSION	AU136409				
KEYWORDS	AU136409.1	GI:10996948			
ORGANISM	human.				
REFERENCE	1 (bases 1 to 784)				
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.				
TITLE	HRI human CDNA project				
COMMENT	Unpublished (2000)				
Genomics Laboratory					
Helix Research Institute					
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan					
Tel: 81-438-52-3951					
Fax: 81-438-52-3952					
Email: genomics@hri.co.jp					
HRI human CDNA project: 5'- & 3'-end one pass s.c. using: Helix					
Research Institute; CDNA library construction: Helix					
Virology, Institute of Medical Science, University of Tokyo, and					
Helix Research Institute.					
Location/Qualifiers					
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/db_xref="taxon:9606"					
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/clone_id="PLACE1"					
/tissue="type="Placenta"					
/note="Vector: pMP18SF1"					
BASE COUNT	247 a 169 c 188 g 174 t				
ORIGIN					

alignment_scores:

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Percent Similarity:	5.162 <td>Gaps:</td> <td>0</td>	Gaps:	0
Percent Identity:	100.000 <td>Percent Identity:</td> <td>99.561</td>	Percent Identity:	99.561

alignment_block:

US-09-649-108-1 x AU136409 ..
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|||||
2 AACATTATTCATTTGTGCATGCAGAGCAAGCAAGCTCAGCATG 51
79 rSerrYrArgGlnArgAlaArgLeuLysAspGlnLeuSerLeuG 96
|||||
52 TACGTCACAGACAGAGGCCCGCGCTGTGAAGACCGCTCCCTGG 101
96 snAlaIleLeuGlnIleThrAspValLysLeuGlnAspAlaGlyVal 112
|||||
102 ATGCTGCACTTCAGATCAGATGATGAATTCAGATGCGAGGCGTAC 151
113 ArgCysMetIleSerTyrGlyAlaAspTyrLysArgIleThrVal 123
|||||
152 CCGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 201

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129 sValasnaIaProTyraenLysIleasnGlnargIleuValasp 146
|||||
202 AGTCAATGCCCATACAAACAAATACCAAAAGAAATTTGGTGGATC 251
|||||
146 rovalThSerGlnHISGluLeuThrCysGlnAlaGluGlyTyrProLys 162
|||||
252 CAGTCACTCTGACATGACATGACATGTGACGCTGAGGGCTACCCCAAG 301
|||||
163 AlaGluValIleTrrPThrSerSerAspHisGlnValLeuSerGlyLysTh 179
|||||
302 GCGGAAGTCATCTGGACAAAGCAGTGCATCAATGCTGAGTGTAAAGC 351
|||||
179 rThrThrThrAsnSerLysArgGluGluLysLeuPheAsnValThrSert 196
|||||
352 CACCAACCAATTCACAAAGAGAGAGAGAGAGCTTTTCAATGTGACCAGCA 401
|||||
196 hrLeuArgIleAsnThrThrThrAsnGluIlePheTyrCysThrPheArg 212
|||||
402 CACTGAGATCAACACAACTAATGAGATTCTTACTGCACTTTTAAAG 451
|||||
213 ArgLeuAspProGluGluAsnHisThrAlaGluLeuValIleProGluLe 229
|||||
452 AGATTAGATTCCTGAGGAAACCATACAGCTGATGTGATCCAGACT 501
|||||
229 uProLeuAlaHisProProAsnGluArgThrHisLeuValIleLeuGlyA 246
|||||
502 ACCTCTGGCAGATCTCCAAATGAAAGGACTCATTGGTAATCTGGGAG 551
|||||
246 IaIleLeuLeuCysLeuGlyValAlaIleLeuThrPheIlePheArgLeuArg 262
|||||
552 CCATCTTTATGCTTGCTGTACACAGTGCATCTCTCGTTTAAAGA 601
|||||
263 LysGlyArgMetMetAspValLysLysCysGlyIleGlnAspThrAsnSe 279
|||||
602 AAAGGAGAGATGATGATGTGAAAAATGTGGCATCCAAAGATACAAACTC 651
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279 rLysLysGlnSerAspThrHisLeuGluGluThr 290
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652 AAAGAGCAAACTGATACATTTGGAGAGAGC 685
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DEFINITION z150f01.y5 Soares ovary tumor NDHOT Homo sapiens cDNA clone
IMAGE:725785 5', mRNA sequence.
AI733919
VERSION 1
VENDOR KODON
SOURCE human.
ORGANISM Homo sapiens
Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
1 (bases 1 to 464)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs: z150f01.s1
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: WashU-NCI human EST project
This read has been verified (found to hit its original self in the
correct orientation)
Putative full length read
The vector to vector length is 544
Insert length: 621 Std Error: 0.00
Seq primer: -40RP from Gibco.
Location/Qualifiers

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:725785"
/clone_1lb="Soares ovary tumor NDHOT"
/sex="Female"
/issue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary: Vector: pT73D (Pharmacia) with a
modified polylinker: site.1: Not 1; site.2: Eco RI; 1st
strand cDNA was primed with a Not 1 - cloning (DT) primer [5'
TGTTACCAATCTGAGTGGAGGCGCGCGGTTTCTTTTCTTTT 3'] ,
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not 1 and cloned into
the Not 1 and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo "
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BASE COUNT 145 a 108 c 105 g 106 t

ORIGIN

alignment_scores:

Quality:	Ratio:	Length:	Gaps:
Percent Similarity: 100.000	5.186	140	0
Percent Identity: 100.000			

alignment_block:

us-09-649-108-1 x AI733919

Align seg 1/1 to: AI733919 from: 1 to: 464

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88 LeuLysAspGlnLeuSerLeuGlyAsnAlaLeuGlnIleThrAspVal 104
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9 TTGAAGAGACACACTCTCCCTGGAAATGCTGCATTCAGATCAGAGACT 58
|||||
104 LysLeuGlnAspAlaGlyValTyrArgCysMetLleSertYrGlyGlyA 121
|||||
59 GAAATTGACAGATGACAGGGGTGTACCGCTGATGATCAGTATGCTGGTG 108
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121 IaAspTyrLysArgIleThrValLysValAsnAlaProTyraenLysIle 137
|||||
109 CCGACTACAGCGAATTACTGTGAAAGTCATATGCCCATACAAACAAATC 158
|||||
138 AsnGlnArgIleLeuValValAspProValThrSerGlnHisGlnLeuTh 154
|||||
159 AACCAAGAAATTTGGTGTGATCCAGTACACCTCTGAAACATGACATGAC 208
|||||
154 rCysGlnAlaLeuGluGlyTyrProLysAlaGluValIleTrrPThrSerSert 171
|||||
209 ATGTGAGGCTGAGGGCTACCCCAAGCCGAAAGTCAATCTGGACAAACACTG 258
|||||
171 sPHisGlnValLeuSerGlyLysThrThrThrThrAsnSerLysArgGlu 187
|||||
259 ACCATCAAGTCTCTGATGTTAAGACACACACACCAATTCCAAGAGAGG 218
|||||
188 GlnLysLeuPheAsnValThrSertThrLeuArgIleAsnThrThrThrAs 204
|||||
309 GAGAGCTTTTCAATGTGACACGACACTGAGAAATCAACACAAACAATVA 358
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204 ngLulePheTyrCysThrPheArgArgLeuAspProGluGluAsnHisT 221
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359 TGAGATTTTCTACTGCACTTTTAAAGAGATTGATCTTGAGGAAACCACTVA 408
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221 hrAlaGluLeuValIlePro 227
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409 CAGCTGAATTTGTCATCCCA 428
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seq_name: gb_est1:AA292201
seq_documentation_block:
LOCUS AA292201 497 bp mRNA EST 08-AUG-1997
DEFINITION z150f01.r1 Soares ovary tumor NDHOT Homo sapiens cDNA clone
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142 CATACAGTGAATGTCATCCCA 119

seq_name: gb_estl:AA896104

seq_documentation_block:

LOCUS AA896104 414 bp mRNA EST 06-APR-1998

DEFINITION vx61903.r1 Stratagene mouse macrophage (#937306) Mus musculus CDNA

clone IMAGE:1279732 5', mRNA sequence.

VERSION AA896104

KEYWORDS

SOURCE

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 414)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MG1:671532

Seq primer: -28m13 rev1 ET from Amersham

High quality sequence stop: 394.

Location/Qualifiers

1. 414

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:1279732"

/clone_lib="Stratagene mouse macrophage (#937306)"

/tissue_type="macrophage"

/dev_stage="MEH1-3 cell line"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: blood; Vector: pluscript SK; Site: 1;

EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. MEH1-3 cell line. Average insert size: 1.5 kb;

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG

3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

COUNT 117 a 102 c 105 g 89 t 1 others

ORIGIN

COUNT 117 a 102 c 105 g 89 t 1 others

COUNT 117 a 102 c 105 g 89 t 1 others

COUNT 117 a 102 c 105 g 89 t 1 others

COUNT 117 a 102 c 105 g 89 t 1 others

COUNT 117 a 102 c 105 g 89 t 1 others

COUNT 117 a 102 c 105 g 89 t 1 others

101 GCAGAGAAAGTGTCCACACTTCCCGACAGAGGAGTGTCTCAATG 150

194 ThrsrThleuarglleasnThrThrThrAsnGluillePherycysth 210

151 ACCAGAGTCTGAGGTCACACGCCACAGCAAGATGTTTCTACGTCAC 200

210 rPhaATGATGleuAspProGluAsnHisThrAlaGluLeuVal111p 227

201 GTATTGAGATCTCACACGCCAGGCGCAAAACACACAGCGGC. GAAATATATC 249

227 roGluLeuProLeuAlaHisProProAsnGluArgThrHisLeuVal111 243

250 CACAGTCTGTCGACACATCTCCACAGACAGATCTGCTGCTGCTGCT 299

244 LeuGluAlaIleuLeuLeuGluGluValAlaLeuThrPhlePha 260

300 CTGGGATCATCTGTTGTCATGATGATGATGATGATGATGATGATG 349

260 glenATGlyGly... ArgMetAspValLysLysCysGly111Gln 276

350 CTGGAGAAACAGTCAAGATGCTAGATGTGAGAAATGTGCTGAGAG 399

276 sPTThrasnSerLys 280

400 ATACAGCTCAAAA 413

seq_name: gb_estl:AA823166

seq_documentation_block:

LOCUS AA823166 510 bp mRNA EST 17-FEB-1998

DEFINITION vx41606.r1 Soaresmammary gland NbMMG Mus musculus cDNA clone

IMAGE:1246402 5', similar to gb:X85991 M.musculus mRNA for

Semaphorin B (MOUSE);, mRNA sequence.

VERSION AA823166

KEYWORDS

SOURCE

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 510)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MG1:660090

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 460.

Location/Qualifiers

1. 510

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:1246402"

/clone_lib="Soares_mammary_gland_NbMMG"

/sex="male"

/tissue_type="mammary gland"

/dev_stage="4 weeks"

/lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT7; Site: 1; Site 2: Eco


```

seq_name: gb_estl:AL537691
seq_documentation_block:
LOCUS      AL537691          857 bp            mRNA           EST       13-FEB-2001
DEFINITION LTI_FlO13_FBnrl Homo sapiens cDNA clone CS0DF026YL01 5
prime, mRNA sequence.
ACCESSION  AL537691
VERSION    AL537691.1 GI:12801184
XREFS
COORDS     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 857)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1..857
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF026YL01"
/dev_stage="LTI_FlO13_FBnrl"
/lab_host="DH10B"
/notes="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA fax : (1) 301 610 8371 Email :
fliang@life tech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT  133 a      291 c      290 g      139 t      4 others
ORIGIN
alignment_scores:
Quality:      267.50      Length:      202
Ratio:        2.140      Gaps:      4
Percent Similarity: 61.881 Percent Identity: 33.168
alignment_block:
US-09-649-108-1 x AL537691 ..
Align seg 1/1 to: AL537691 from: 1 to: 857
15 LeuleuAsAlapherThyValThrValPolysAsPleuTyValValol 31
|||||:::|||||::: ||| |||||:::||||| |||:::
265 CTCACGAGGAGCCCTCGAGGTCCAGGTCCTGAAGAACCAGTGATGCACCT 314
31 uTYrGysrAsnMetThrIlleGlucLysrSpheProValGluYsgInL 48
|||||:::|||||::: |||||:::||||| |||:::
315 GGtGGGACCGAATGCCACCTGCTGCTCTCTCTCTCCCTGAGCCTGGACT 364

```

[illegible]

/note="Vector: PCWSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCWSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 150 a 274 c 277 g 147 t 1 others
ORIGIN

alignment_scores:
Quality: 265.00 Length: 224
Ratio: 1.893 Gaps: 6
Percent Similarity: 59.829 Percent Identity: 32.051

alignment_block:
9-649-108-1 x AL545252 ..

Align seg 1/1 to: AL545252 from: 1 to: 849

```

15 LeuLeuAaAlaPheThrValThrValProLysAspLeuTyrValValG1 31
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
128 CTCACAGAGAGCCCTGGAGGCTCCCTGAGAGCCAGGAGGAGGAGGCT 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
31 UTyGlySerAsnMetThrIleGlyLysPheProValGlyGlyGlnL 48
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
178 GGTGGGACCGATGCCACCCTGCTGCTCTCTCTCTCTCTCTCTCTGCT 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48 euAspLeuAlaAlaLeuIleValTyrTrpGluMetGluAspLysAsnIle 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
228 TCAGGCTGGACAGCTCAACCTCATCTGGAGCTGACAGATGCCAA... 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 IleGlnPheValHisGlyGluGlnAspLeuLysValGlnHisSerSerty 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
275 ..CAGCTGGTGACACGCTTGGCTGAGGGCCAGGACGAGGCGGCTTA 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
81 rArgGlnrGAlaArgLeuLeuLysAspGlnLeuSerLeuGlnAsnAla 98
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
322 TGCCACGCGCAGGCGCTCTTCTGACCTGCTGACACGAGGACGACGCT 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
98 lAlaGlnIleThrAspValLysLeuGlnAspAlaGlyValTyrArgCys 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
372 CCCTGAGCTGGACAGCGTGGCTTTGGGAGCAGGAGGAGCTTACCTTC 421
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
115 MetIleSerTyrGlyAlaAspTyrLysArgIleThrValLysValAs 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
422 TTCGTGAGCATCCGGGATTTGGGACGCGCTGCCGTGACCTGACAGTGGC 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
131 nAlaProTyrAsnLys.....IleAsnGlnArgIleL 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
472 CGCTCCCTACCTGAGAGCCAGCATGACCTGAGCCCAAGAGGACCTGC 521
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
142 euValValAspProValThrSerGlnHisGlyLeuThrCysGlnAla... 157
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
522 GGGCCGGGACATGGTGAC.....ATCAGCGTCCAGCTAC 559
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
158 GluGlyTyrProLysAlaGluValIleThrPheSerSerPheHisGln 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
560 CAGGCGTACCTGAGGCTGAGGTTCCTGGCAGGATGGGACAGGCTGTCC 609
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
174 lLeuSerGlyLysThrThrThrThrAsnSerLysArgGluGlyLysLeu 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
610 CCTGACTGGACAGTGCACGCTCGACATGCCAAGAGGAGGCTGTGT 659
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
191 heAsnValThrSerThrLeuArgIleAsnThrThrThrAsnGluIlePhe 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
660 TTGATGTGCACAGCATCTCGGGGTGTGTGTGTGTGTGTGTGTGTGTGT 709
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
208 TyGlyThrPheArgArgLeuAspProGluLysHisThrAlaGluLe 224

```

```

710 AGCTCCGTGGTGGCAGCCGCTGCTGACAGAGGAGCCACAGCT..... 754
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
224 uValIleProGluLeuProLeuAlaHisPro.....ProAsnGlu 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
755 .....CTGTCAACATACACCCAGAGAGAGCCACAGAGAGC 791
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
238 Tg 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
792 GG 793

```

seq_name: gb_est1:AL584057

seq_documentation_block:

```

LOCUS AL584057 683 bp mRNA EST 28-FEB-2001
DEFINITION AL584057 Stragene Chick Embryo Lambda cDNA library (* 937405)
GALLUS gallus CDNA clone ROS003B03, mRNA sequence.
ACCESSION AL584057
VERSION AL584057.1 GI:13162788
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 683)
REFERENCE
AUTHORS Murray,F.
TITLE Stragene Chick Embryo Lambda cDNA library
JOURNAL Unpublished (2001)
COMMENT
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
Seq primer: T3.

```

FEATURES

source

Location/Qualifiers

```

1..683
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS003B03"
/clone_1db="Stragene Chick Embryo Lambda cDNA library (*
937405)"

```

```

/tissue_type="Embryo"
/dev_stage="5 days old"
/lab_host="SOLR cells (kanamycin resistant)"

```

```

/note="vector: p Bluescript SK+ Site_1: EcoRI; Site_2: XhoI
; Cloned unidirectionally. Primer: Oligo dT, Uni-ZAP XR
vector. Average insert size: 1.5kb.; 5' adaptor sequence:
5' GAATTGGGACGAG 3'; 3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTTCTTTT 3'"

```

BASE COUNT 220 a 124 c 165 g 170 t 4 others
ORIGIN

alignment_scores:
Quality: 263.00 Length: 117
Ratio: 2.922 Gaps: 1
Percent Similarity: 76.923 Percent Identity: 46.154

alignment_block:
US-09-649-108-1 x AL584057 ..

Align seg 1/1 to: AL584057 from: 1 to: 683

```

110 GlValTyrArgCysMetIleSerTyrGlyAlaAspTyrLysArg11 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3 GGGCTTACNATTGCCATTATGAGATGGGAGCTGACTACAGAGCCAT 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
126 eThrValLysValAsnAlaProTyrAsnLysIleAsnGlnArgIleLeu 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 CAATGTGAAGTTCAGGCTCTTACAGAGCATATAACCAAGAA.....G 96

```


Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
source
1.793
Location/Qualifiers

BASE COUNT 224 a 217 c 163 g 183 t 6 others
ORIGIN
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1003145"
/clone_id="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL3"

alignment_scores:
Quality: 243.50 Length: 176
Ratio: 2.136 Gaps: 7
Percent Similarity: 64.773 Percent Identity: 39.773

alignment_block:
09-649-108-1 x AU135908 ..

Align seg 1/1 to: AU135908 from: 1 to: 793

```

112 TTTATGTCyMetileSerTyrglyala...AspTyrglyargileth 127
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 TACCAATGATATATCATCTATGCGGCTGGAGCTACAACTACCTGAC 51
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
127 TValysValasnaIaIaProTyraNlysIleasnIlnatgIleValy 144
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
52 TCTGAAGTCAAGAGCTCTCTACAGAGAAATAAACATCAATCCAAAG 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 aIAspProvalThrserGluNhsIgluLeuThrcysGlnIlnatgIlyr 160
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
102 TT...CCAGAAACAGATGAGTAGAGCTACCTGCCAGCTACAGTTAT 148
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
161 ProlysAlaIgluValIleTrpThrserSerAspNhsIgluValleuSer 177
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
149 CCTGTGGCAGAGTATCTCTGCCAAG.....GTCCAGCCT 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
177 yLysThrThrThrAsnSerLysArgIluGluLysLeuPheAsnValT 194
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 TCTCTCCCAACACAGCCACCTCCAGAGCCCTGAGAGCCTCTCCAGGTCA 233
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
194 hSerThrleuArgIleasnThrThrAsnIluIlePheTyrcysThr 210
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
234 CCAGTGTCTGTGGCCTAAAGCCACCCCTGGCAGAACTTCAGCTGTGTG 283
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
211 PheArgArgLeuAspProIluGluAsnIsthraIgluLeuValIlePr 227
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
284 TTC.....TGCATATCTCAGCGAGGAACTTACTTTGGC 318
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
227 ocIleuProleuAlaIhIsProProAsnIluArgThrIhIsleuValIle 244
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 GCGCATGACCTTCAAGTCAAGATGAAAGCCCAAGCCATCCAACTTGGC 368
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 euGIyAlaIleleu.....CysLeuGIyAlaIleuThrPheIle 258
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
369 TGCTTACATTTTCATCCCTCTCTGATC...ATTCCTTTTCATTTTCANA 415
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
259 PheArgLeuArgLysGIyArgMetet.AspValLysLysCysGIyIleG 275
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
416 GCCACAGATGATGCCCTAAGAAACAAACACTGTCTCAAAAGCTGTATTTTC 465
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
275 InAspThrAsnSerLysLysGlnSer 283
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
466 AAAAGCACACAAACAAAGACCTGTCA 491
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

seq_name: gb_est1:BE367954

seq_documentation_block:

LOCUS BE367954 750 bp mRNA EST 21-JUL-2000
DEFINITION 601221824F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3591004 5',

ACCESSION BE367954
VERSION BE367954.1 GI:9313317
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LM8759 row: 0 column: 05
High quality sequence stop: 527.

FEATURES
source
1.750
Location/Qualifiers

BASE COUNT 232 a 165 c 218 g 135 t
ORIGIN
/organism="Mus musculus"
/strain="C57BL/6J (f1)"
/db_xref="taxon:10090"
/clone="IMAGE:3591004"
/clone_id="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
stem cell origin."
/lab host="DH10B"
/note="Organ: lung. Vector: pCMV-Sp6X6. Site: J. Salt.
Site_2: Notti. Cloned unidirectionally. Primer: Oligo dT.
Library constructed by: Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

alignment_scores:
Quality: 242.50 Length: 154
Ratio: 2.109 Gaps: 12
Percent Similarity: 74.675 Percent Identity: 48.701

alignment_block:
US-09-649-108-1 x BE367954 ..

Align seg 1/1 to: BE367954 from: 1 to: 750

```

149 SerGluNhsIgluLeuThrcysGlnIlnatgIlyrProlysAlaIly 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 TCTGAGCATGAAGTATCTGTGAGCCGAGGGATATCCAGAGCTGAGG 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
165 aIleTrpThr.SerSerAspNhsIgluVal.LeuSerGlyLysThrThr 181
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
54 TATCTGGACAAACAGGTGACCGGCAAGCCGTGTGGGAAGATGAGAG 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 hThrAsnSerLysArgIluGluLysLeuPheAsnValThr.....Ser 195
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
104 TGTCCACACCTTACCGGACAGAGGGGATGCTTCAACTGTGAGGACG 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 ThrLeuArg.IleasnThrThrAsnIluIlePhe..TyrcysThrP 211
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 AGTCTGAGGGGTCAAGCCAGATGCATAATGATGTTTCGTACTGTACT 203
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
211 hArgArgLeu.AspProIlu.GluAsnIsthraIgluLeuValIlePr 227
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
204 GTGGGAGATCAGACGCCAGGCGCAACACACACAGACAGCTGATCTCC 253
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
227 to.GluLeuProleuAlaIhIsProProAsnIluArgThrIhIsleuVal 243
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


CC which are useful for treating immunological disorders, such as autoimmune
 CC diseases e.g., heart disease, myocardial infarction and atherosclerosis
 CC or in the case of inhibiting rejection of transplants. These fusion
 CC proteins are also used as immunogens to produce anti-B7-4 antibodies.
 CC B7-1 is useful in promoting the maintenance of pregnancy. B7-4 protein is
 CC highly expressed in placental trophoblasts and plays a role in preventing
 CC maternal rejection of the foetus. B7-4 cDNA is also useful for
 CC gene mapping.

XX
 XX Sequence 1552 BP; 466 A; 312 C; 384 G; 390 T; 0 other:

Alignment_scores:

Quality: 1511.00 Length: 290
 Ratio: 5.210 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-649-108-1 x AAD02773 ..

seg 1/1 to: AAD02773 from: 1 to: 1552

```

1 MetAgtlIlePheAlaValPheIlePheMetHrTyrrTprHisLeuLeuAs 17
|||||
53 ATGAGGATATTTGCTGCTTATATTCATGACCTAGCTGCGCATTCCTGAA 102
|||||
17 nAlaPheThrValThrValProLysAspLeuTyrrValValGluTyrgLys 34
|||||
103 CGCATTTACTGTCACGCGTTCCCAAGACCTATATGTGGTAGGATGGGA 152
|||||
34 eAsnMetThrIleGluCysLysPheProValGluLysGlnLeuAspLeu 50
|||||
153 GCATATATACAAATGAAATCCAGTAGAATAAACAATATAGACCTG 202
|||||
51 AlaAlaLeuIleValTyrrProLysMetGlnAspLysAsnIleLeuLph 67
|||||
203 GCTGCACATATTTGTTATTTGGAAATGGAGGATAGAAACATTATTCATT 252
|||||
67 eValHisGluGlnAspLeuLysValGlnHisSerSerTyrrArgGlnA 84
|||||
253 TGTGCGATGAGAGGAAAGACCTGAAGCTTCAGCATGATGACACAGAGA 302
|||||
84 rGAlaIleGluLeuLysAspGlnLeuSerLeuGlnAsnAlaIleLeuGln 100
|||||
303 GGGCCGGCTGTTGAAGACCAACGCTCTCCGGAATGCTGCACCTTCAG 352
|||||
101 IleHrAspValLysLeuGlnAspAlaGlyValTyrrArgCysMetIleSe 117
|||||
53 ATCACAGATGTGAATTCAGAGATCAGGGGTGATCCGCTCATCATCAG 402
|||||
117 rTyrrGlyAlaAspTyrrLysArgIleHrValLysValAsnAlaProT 134
|||||
403 CTATGCTGTGGCGGCTACAAAGCGAATTACTGTGAAGCAATGCCCAT 452
|||||
134 yrrAsnLysIleAsnGlnArgIleLeuValValAspProValThrSerGlu 150
|||||
453 ACAACAAATCAACCAAGAAATTTGGTGTGATCCAGTCAACCTCTGAA 502
|||||
151 HisGluLeuThrCysGlnAlaGluGlyTyrrProLysAlaGlnValIleTr 167
|||||
503 CATGAACTGACATGTCAGGCTGAGGGCTAACCCCAAGGCCGAAGTATCTG 552
|||||
167 pThrSerSerAspHisGlnValLeuSerGlyLysThrThrThrAsnS 184
|||||
553 GACAGAGCTGACATCAAGTCTCAGTGTGAAGACCAACACCAACCAAT 602
|||||
184 eLysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
|||||
603 CCAAGAGAGAGAGAAAGCTTTTCATGTGACCAACACACTGAGATCAAC 652
|||||
201 ThrThrThrAsnGluIlePheTyrrCysThrPheArgArgLeuAspProL 217
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653 ACAACAACTAATGAGATTTTCTACTGCACTTTTAGGACATTAGATCTCGA 702

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seq_name: /SID52/gcdata/geneseq/geneseq/NA2001.DAT: AAD02708

seq_documentation_block:

ID AAD02708 standard; cDNA; 1553 BP.

AC AAD02708;

DT 31-MAY-2001 (first entry)

XX Human B7-4 membrane (B7-4M) protein cDNA.

XX Human; B7-4 membrane protein; B7-4M; chromosome 9; antiviral; Influenza;

KW immunomodulatory; acquired immune deficiency syndrome; AIDS; anti-tumour;

KW graft-versus-host disease; GVHD; immunological disorder; Herpes disease;

KW autoimmune disease; common cold; shingles disease; encephalitis; therapy;

KW organ transplant; gene mapping; transgenic; viral infection; SS.

OS Homo sapiens.

XX Key

FT CDS

FT sig_peptide

FT mat_peptide

FT product= "Mature human B7-4 membrane (B7-4M) protein"

XX WO200114556-A1.

XX 01-MAR-2001.

XX 23-AUG-2000; 2000MO-US23256.

XX 23-AUG-1999; 99US-0150390.

XX (DAND) DANA FARBER CANCER INST INC.

XX Freeman G, Boussiotis V, Chernova T, Malenkovich N;

XX WPI; 2001-202936/20.

XX P-PSDB; AAY72645.

XX New human B7-4 polypeptides useful for enhancing the immune response

XX PT against a viral infection or induce a tumor immunity and to diagnose

XX PT conditions related to aberrant B7-4 expression or activity

XX Claim 1; Fig 2; 123pp; English.

XX The present cDNA sequence encodes human B7-4 membrane (B7-4M) protein

XX having a transmembrane and short cytoplasmic domain. Human B7-4 protein


```

PF 01-NOV-2000; 2000MO-US30039.
XX
XX 09-NOV-1999; 99US-0164344.
PR 07-APR-2000; 2000US-0195296.
PR 27-JUL-2000; 2000US-0221367.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Olisen HS, Komatsoulis G, Duan DR, Ebner R, Ruben SM;
XX WPI: 2001-308780/32.
XX P-PSDB; AAE01164.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
XX PT used in preventing, treating or ameliorating a medical condition
XX
XX PS Claim 1; Fig 1; 474pp; English.
XX
XX AAD05053-AAD05106 represent cDNAs corresponding to 15 human secreted
XX C protein genes, and AAE01164-AAE01217 represent the proteins they encode.
XX C AAE01218-AAE01226 represent human secreted protein fragments or variants.
XX C The secreted proteins and their genes are useful for preventing,
XX C treating or ameliorating medical conditions, e.g., by protein or gene
XX C therapy. Pathological conditions can be diagnosed by determining the
XX C amount of the new protein in a sample or by determining the presence of
XX C mutations in the new genes. Specific uses are described for each of the
XX C 15 genes, based on the tissues in which they are most highly expressed,
XX C and include developing products for the diagnosis or treatment of
XX C proliferative disorders, cancer, tumors, foetal and developmental
XX C abnormalities, haematopoietic disorders, diseases of the immune system,
XX C AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX C allergies, neurological disorders (e.g., Alzheimer's disease,
XX C Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX C skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX C cardiovascular disorders, angioendothelial disorders, kidney disorders,
XX C gastrointestinal disorders, pregnancy-related disorders, endocrine
XX C disorders, and infections. The proteins can also be used to aid wound
XX C healing and epithelial cell proliferation, to prevent skin aging due to
XX C sunburn, to maintain organs before transplantation, for supporting cell
XX C culture of primary tissues, to regenerate tissues, to identify their
XX C cognate ligands or binding partners, and in chemotaxis, and can be used
XX C as a food additive or preservative to modify storage properties.
XX C Antibodies specific for a protein of the invention can be used in
XX C alleviating symptoms associated with the disorders mentioned above, and
XX C in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
XX C immunosorbent assay (ELISA). The present sequence represents a human
XX C secreted B7-H6 protein-encoding cDNA of the invention.
XX
XX Sequence 3568 BP; 1017 A; 720 C; 738 G; 1090 T; 3 other:

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Alignment_scores:
  Quality: 1511.00      Length: 290
  Ratio: 5.210          Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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Alignment_block:
us-09-649-108-1 x AAD05053

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Align seg 1/1 to: AAD05053 from: 1 to: 3568

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1 Metatglllephaalalalpheilephemeethrtyrrphisleuleuas 17
  |||||||
62 ATGAGGATATTGGCTGCTCTTATATTGACCTACTGCGCATTTCTCTGAA 111
  |||||||
17 nalaphethrvalthrvalprolysaspleuetyrvalvalglutyrlys 34
  |||||||
112 GCGATTTCGTGACGAGGTTCCAGAGACCTATATGTGGTAGATGGGA 161
  |||||||
34 eTasmetthrileglucylslyspheprovalglulysglinleuaspleu 50
  |||||||
162 GCAATATGACAAATTCGAAATTCGCCAGTAGAAGAAACAATTAACCTCG 211
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51 Alalaleuilevaltyrrpqlumetgluasplysasniletleghlnh 67
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212 CCGCACTAATTGCTATTGGAAATGAGAGATAGAACATATATTCATTT 261
  |||||||
67 eValhislglucluaspleuleysvalglinhlsersertryrarglva 84
  |||||||
262 TGTGCATGAGAGAGAAAGACCTGAAGTTTCAGCATATGCTACAGACCA 311
  |||||||
84 rgalAargleuleuleysaspclnleuserleuglyAsnalAlaleuIn 100
  |||||||
312 GGGCCCGGCTGTGAAAGACCAAGCTCTCCCTGGGAAATGCTGCATTCG 361
  |||||||
101 lIethrAspvalysleuGlaspAlaaglyValTyrrArgCysMetIleSc 117
  |||||||
362 ATCACAGATGTGAATTCAGAGATCCAGGGGCTACCCGCTCATGATCAG 411
  |||||||
117 rTyrrGlglYAlaAspyTyrrlysrArgIlethrVallysValnsAlaProT 134
  |||||||
412 CTATGTGTGTCCGCTACCAAGCGAATTCGTGAAAGTCAATGSCCAT 461
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134 yrasnlyslleasnlnarglileuValvalaspProvalThrserglu 150
  |||||||
462 ACAACAAATCACCAAGAATTTGGTTGGATCCAGTCCCTCTGAA 511
  |||||||
151 HislgluleuthrCysglAlaaglytyrrprolysalagluvallethr 167
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512 CATGAACCTGACATCTCAGCGAGGCGTACCCCAAGGCGGAATATCTG 561
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167 pThrserSerAspHisglInvalleuSerGlylysrThrThrThrThrAns 184
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562 GCAAGACGCTGACATCAAGTCTGAGTGTAAGACCAACCAACCAATTT 611
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184 eTlysrArgglulglulysleupheasnValThrSerThrleuArgIleasn 200
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612 CCAAGAGAGAGAGAAAGCTTTTCATGTGACACAGACACTGAGAAACAG 661
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201 ThrThrThrAsnGlulIlePheThrCysThrPheArggluasProgl 217
  |||||||
662 ACACACATTAATGACATTTTCTACGCACTTTTACGACATTAATGATCTGA 711
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217 uGlusnHlsThrAlaGluleuValIleProgluleuProleuAlaHlsP 234
  |||||||
712 GGAACCATACAGCTGATTTGGTTCATCCACAGACTCTCTGGCACATC 761
  |||||||
234 rOProAsnGluarGThrHlsleuValIleleuglyAlaIleleuleucys 250
  |||||||
762 CTCCAATGAAGAAGACCTCCTGTAATTCGGAGCCATCTATATATCC 811
  |||||||
251 leuglyValAlaleuthrPheIlePheargleuATglysGlyArgmethe 267
  |||||||
812 CTGGGTGTAGCACTGACATTCATCTCCGTTTAAAGAAAGGAGATATGAT 861
  |||||||
267 lAspValIlyslsCysGlyIleGlAspThrAsnSerlyslsGlnSerA 284
  |||||||
862 GCATGTGAAAAAATGTGGCATTCAGATACAAACTCAAGAAAGCAAGAGTG 911
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284 sPTThrHlsleuGlulgluthr 290
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912 ATACACATTTGGAGCAGACG 931
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AA502076

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seq_documentation_block:
ID_AA502076 standard: cDNA; 3575 BP.

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XX AC AA502076;
XX
XX DT 18-JUL-2001 (first entry)
XX
XX DE Human TANGO 509 cDNA sequence.
XX
XX KW Human: TANGO 509; transmembrane protein; diagnostic; asthma;
KW Immunological disorder; arthritis; graft rejection; renal disorder;

```


KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
KM AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
KW neurodegenerative disease; Parkinson's disease; ss.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 59..931
FT /tag= a
FT /product= "TANGO 509"
FT /note= "The coding sequence (ORF) is specifically
FT sig_peptide 59..112 claimed in Claim 1"
FT /tag= b
FT mat_peptide 113..929
FT /tag= c
XX
XX W0200121631-A2.
XX
XX P 29-MAR-2001.
XX
XX PF 20-SEP-2000; 2000WO-US25982.
XX
XX PR 20-SEP-1999; 99US-0399723.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;
XX
XX DR WPI: 2001-211461/21.
XX P-PSDB: AAU01362.
XX
XX PT New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO
XX 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
XX PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
XX PT disease -
XX
XX PS Claim 1; Fig 22; 362pp; English.
XX
XX CC The sequence represents the coding sequence of human TANGO 509
XX CC transmembrane protein. The nucleic acid and polypeptide sequences
XX CC are useful for the diagnosis, prognosis and treatment of immunological
XX CC disorders (e.g. arthritis, graft rejection and acquired immunodeficiency
XX CC syndrome), inflammatory disorders (e.g. psoriasis and asthma), renal
XX CC disorders, embryonic disorders, brain-related disorders (e.g. cerebral
XX CC oedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate-
XX CC related disorders, pituitary-related disorders (e.g. Cushing's disease)
XX CC and neurodegenerative diseases (e.g. Parkinson's disease).
XX
XX Sequence 3575 BP; 1029 A; 717 C; 738 G; 1091 T; 0 other:
50
alignment_scores:
Quality: 1511.00 Length: 290
Ratio: 5.210 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-649-108-1 x AAS02076 ..
Align seg 1/1 to: AAS02076 from: 1 to: 3575
1 MetatglllephalaValaPheIlePheMethtTyrTTPHISleuLeuAs 17
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59 ATGAGGAAATTTGCTGTCTTATATTCATGACCTACTGCAATTCCTGAA 108
17 nalaPheThValThValProLysAsPLeuTyrValValGluTyrGlys 34
|||||
109 CGCATTTACTGTACGGTTCCCAAGACCTATATGTGTGAGAGTATGGA 158
34 eTAsMethtTleGluCysLysPheProValGluLysGlnLeuAsPLeu 50
|||||

159 GCATATGCAATTTGAATGCATTAATTCAGTAGAAAAACAAATAGACCTG 208
51 AlaaIalaLeuIleValIlyTTPGImetGluAsPlysAsnIleIleGlnPh 67
|||||
209 GCTGCACATTAATGTCYATTTGGGAAATGAGAGATTAAGAACATTAATCAAT 258
67 eValHISGlyGluGluAsPLeuLysValGlnHISerSerTyrArgGln 84
|||||
259 TGTGCTGGAGAGAGAACCTGAGGTTCCAGCTTAGTACTACAGACAGA 308
84 rGAlaArgLeuLeuLysAsPGLnLeuSerLeuGlyAsnAlaIalaGln 100
309 GGGCCCGCTGTTGAAGAGACACCTCCCTGGGAATGCTGCACCTCAG 358
101 lIeThAsPValLysLeuGlnAsPAlaGlyValIlyTyrArgCysMetIleSe 117
|||||
359 ATCAGAGATGTGAATTTGAGGATGAGGAGGCTTACCGCTGCATGATCAG 408
117 rTYrGlyGlyAlaAsPTrLysArgIleThValLysValAsnAlaIaPTr 111
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409 CTATGCTGCTGCGGACTACAGCGAATTTACTGTGAAGTCATATGCCCAT 458
134 yTAsnLysIleAsnGlnArgIleLeuValAlaAsPProValThrSerGlu 150
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459 ACACAAATCAACCAAGAAATTTGTTGTGATCCAGTCACCTCTGAA 508
151 HIsGluLeuThrCysGlnAlaGluGlyTyrProLysAlaGluValIleTr 167
|||||
509 CATGAACCTACATGTCAGGCTGAGGCTACCCCAAGCCGCAACTCATCTG 558
167 pThrSerSerAsPHisGlnValLeuSerGlyLysTrhThThThAsn 184
|||||
559 GACACACAGTACCATCAAGTCTGAGTGTAGAGACACACCAACCAAT 608
184 eTlysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
|||||
609 CCAGAGAGAGAGAGAGCTTTTCAATGTGACCGACACATGAGAAATCAC 658
201 ThThThThAsnGluIlePheTyrCysThrPheArgArgLeuAsPTrCG 217
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659 ACACACACTTAATGAGATTTTCTACTGCTCTTTAGAGATTAATGATCTGA 708
217 uGluAsnHISThrAlaGluLeuValIleProGluLeuPLeuAlaHISp 234
709 GGAAGAACATACAGCTGATTTGCTATCCCAAGACATACCTGTGCACAT 758
234 rOProAsnGluArgThrHISLeuValIleLeuGlyAlaIleLeuLeuCys 250
|||||
759 CTCCAATGAAGAGACTCTTGTAATCTGGAGCCCATCTTAATATGC 808
251 LeuGlyValAlaLeuThrPheIlePheArgLeuArgLysGlyArgMetWe 267
|||||
809 CTTGCTGTAGCACTGACATTCATCTTCGTTAAAGAAAGGAGAAATGAT 858
267 lAsPValLysLysCysGlyIleGlnAsPThrAsnSerLysGlnSerA 284
859 GGATGTGAAAAAATGTGCGATCCCAAGATACAAACTCAAGACAGCAAGTC 908
284 sPThrHISLeuGluGluThr 290
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909 ATACACATTTGGAGAGACG 928
seq_name: /SIDS2/gcdata/geneseq/geneseq/NA2001.DAT:AAS05592
seq_documentation_block:
ID AAS05592 standard: cDNA: 3616 BP.
XX
XX AAS05592:
AC
XX
XX 26-SEP-2001 (first entry)
DT
XX
XX Human immunoregulatory protein B7-H1 cDNA sequence.
DE
XX

KW Human: immunoregulatory protein; B7-H1; co-stimulating T-cell;
 KW B-cell antibody-producing response; IgG2a antibody response; APC;
 KW Immunodeficiency disease; inflammatory disease; autoimmune disease;
 KW antigen presenting cell; pathologic cell mediated disease; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 73..945

FT /*tag- a

FT /*product- "B7-H1 protein"

FT sig_peptide 73..138

FT /*tag- b

FT mat_peptide 139..942

FT /*tag- c

PN WO200139722-A2.

PD 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US32583.

PR 30-NOV-1999; 99US-0451291.

PR 28-AUG-2000; 2000US-0649108.

PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PI Chen L;

XX WPI: 2001-397926/42.

DR P-PSDB; AAU03559.

XX Novel DNA encoding immunoregulatory molecule B7-H1, is useful for

PT co-stimulating a T cell for augmenting immunoregulation and for

PT controlling pathologic cell mediated conditions -

PS Example 2: Fig 1; 85pp: English.

XX The present sequence encoding for novel human immunoregulatory protein
 CC B7-H1 (B7-H1) is capable of co-stimulating T-cells. The sequence for
 CC mouse B7-H1 (mB7-H1) is also given (AAU03560). B7-H1 is useful for
 CC co-stimulating T-cells such as helper T-cells that provide helper
 CC activity for B-cell antibody-producing response e.g. IgG2a antibody
 CC response. In a mammal having an immunodeficiency disease, inflammatory
 CC condition or an autoimmune disease, by culturing B7-H1 with the
 CC mammalian T-cells in vitro, or administering B7-H1 or a nucleic acid
 CC encoding B7-H1 to the T-cells, such that the level of CD40 ligand on the
 CC T-cell surface is increased. The method further involves providing a
 CC recombinant cell e.g. an antigen presenting cell (APC) which is the
 CC progeny of a cell obtained from the mammal and has been transfected or
 CC transformed ex vivo with a nucleic acid encoding B7-H1, so that the cell
 CC expresses B7-H1, and administering the cell to the mammal. Prior to
 CC administration, the APC is pulsed with an antigen or an antigenic
 CC peptide. B7-H1 can be used to control pathologic cell mediated
 CC conditions (e.g. those induced by infectious agents such as Mycobacterium
 CC tuberculosis) or other pathologic cell mediated responses such as those
 CC involved in autoimmune diseases (e.g. rheumatoid arthritis).

XX Sequence 3616 BP; 1059 A; 726 C; 739 G; 1092 T; 0 other;

alignment_scores:

Quality: 1511.00 Length: 290
 Ratio: 5.210 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-649-108-1 x AAS06592

Align seg 1/1 to: AAS06592 from: 1 to: 3616

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73 ATGAGGATATTGGCTGCTTTATATTACATGACCTAGCCATTTTCGAA 122
 17 nAlaPheThrValThrValProLysAspLeuTyrrValGluTyrrGlys 34
 ||||||||||||||||||||||||||||||||||||||||||||
 123 CGCATTACTGTCACGGTTCCACAGGACCTATATGTTGGTAGATGTA 172
 34 eAspMetThrIleGluCysLysPheProValGluLysGlnLeuAspLeu 50
 ||||||||||||||||||||||||||||||||||||||||||||
 173 GCAATATGACAAATTCGAAATTCACGATTAACAAATTCGACCTG 222
 51 AlaAlaLeuIleValTyrrTrpGluMetGlnAspLysAsnIleGlnPh 67
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 223 GCTGCACTAATTGCTATTGGAATGAGATTAAGACATTATTCATTT 272
 67 eValHisGlyGluGluAspLeuLysValGlnHisSerSerTyrrArgGln 84
 ||||||||||||||||||||||||||||||||||||||||||||
 273 TGTGATGAGAGGAGACCTGAAAGTTCCAGCATAGTACACACACGA 322
 84 rGlaIArgLeuLeuLysAspGlnLeuSerLeuGlyAsnAlaAlaLeuGln 1004
 ||||||||||||||||||||||||||||||||||||||||||||
 323 GGGCCGGCTGTGAAAGACAGCTCTCCGTGGAAATGCTGCATTCAG 372
 101 IleThrAspValLysLeuGlnAspAlaGlyValTyrrArgCysMetIle 117
 ||||||||||||||||||||||||||||||||||||||||||||
 373 ATCACAGATGTGAATTCAGAGATCAGGGGTGTACCCCTGATGATCAG 422
 117 rTyrrGlyAlaAspTyrrLysArgIleThrValLysValAsnAlaProV 1344
 423 CTATGCTGTGCGCCGACTCAAGCGAATTAAGTGAAGTCATATGCCCAT 472
 134 yAsnLysIleAsnGlnArgIleLeuValValAspProValThrSerGln 150
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 473 ACAACAAATCAACCAAGAAATTTGGTGTGAGACAGTCAACCTGAA 522
 151 HisGluLeuThrCysGlnAlaGluTyrrProLysAlaGluValIleGln 167
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 523 CATGAACTGACATGTCACGCTGAGGCTACCCCAAGGCCGAATATCTG 572
 167 pThrSerSerAspHisGlnValLeuSerGlyLysThrThrThrAsn 184
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 573 GACAAAGAGTGCATCAAGTCTGAGTGTAAAGACACACCAACCATTT 622
 184 eLysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
 ||||||||||||||||||||||||||||||||||||||||||||
 623 CCMAAGAGAGAGAAAGCTTTCAATGTGACACACACCTGAGATTCAC 6724
 201 ThrThrTrpAsnGluIlePheTyrrCysThrPheArgLeuAspProGln 217
 ||||||||||||||||||||||||||||||||||||||||||||
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 ||||||||||||||||||||||||||||||||||||||||||||
 723 GGAAACCATATGACGCTGATTTGGTCATCCAGAACTACCTGTGCACAT 7724
 224 rOPrAsnGluArgThrHisLeuValIleLeuGlyAlaIleLeuLeuGly 257
 ||||||||||||||||||||||||||||||||||||||||||||
 773 CTCCAAAATGAAGACCTCCTGTAATTCGGGAGCCATCTTAATTAAGC 822
 251 LeuGlyValAlaLeuThrPheIlePheArgLeuArgLysGlyArgMetLe 267
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 823 CTGGGTAGCAGCTGACATTCATCTTCGCTTTAAGAAAAGGAGATATAT 872
 267 tAspValLysLysCysGlyIleGlnAspThrAsnSerLysLysGlnSerA 284
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 873 GGATGTGAATAAATGTGCTATCCAAAGATACAAACCAAGAAAGCAACTG 9224
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 923 ATACACATTTGAGAGAGACG 942

seq_name: /STDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.AAS02118

seq_documentation_block:

ID AAS02118 standard; cDNA: 3575 BP.
XX
AC AAS02118;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human TANGO 509, alternative cDNA sequence #1.
XX
KW Human: TANGO 499; transmembrane protein; diagnostic; asthma;
KW Immunological disorder; arthritis; graft rejection; renal disorder;
KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
KW neurodegenerative disease; Parkinson's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..931
FT /tag= a
FT /product= "TANGO 509, alternative transmembrane
protein #1"
XX
XX W0200121631-A2.
XX
XX 29-MAR-2001.
XX
XX 20-SEP-2000; 2000MO-US25982.
XX
XX 20-SEP-1999; 99US-0399723.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;
XX
XX DR WPI: 2001-211461/21.
XX
XX P-PSDB: AAU01407.
XX
XX PT New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO
PT 351, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease.
XX
XX PS Disclosure: Page 342-344; 362pp; English.
XX
XX CC The sequence represents the coding sequence of human TANGO 509,
CC alternative transmembrane protein #1. The nucleic acid
CC and polypeptide sequences are useful for the diagnosis, prognosis and
CC treatment of immunological disorders (e.g. arthritis, graft rejection and
CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.
CC ischaemia), tumours, prostate-related disorders, pituitary-related
CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
CC Parkinson's disease).
XX
XX SQ Sequence 3575 BP; 1030 A; 717 C; 738 G; 1090 T; 0 other;

alignment_scores:
Quality: 1508.00 Length: 290
Ratio: 5.200 Gaps: 0
Percent similarity: 100.000 Percent identity: 99.655

alignment_block:
US-09-649-108-1 x AAS02118
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59 ATGAGGATATATGCTGTCTTTATATTCATGACCTACTGCAATTGCTGAA 108

17 nalapehtrValThrValProlysAspleuTyrrValIgluTyrcys 34
|||||
109 CGCATTTACTGTCACGGTTCCAAAGGACCTATATGTGTAGTATGTA 1*
34 erasmetThrIleglucysLysPheProvalGluysGlnleuAspleu 50
|||||
159 GCAATATGACAAATTGAATGCAAAATTCCTCCATAGAAAAACATTAAGCC 208
51 AlaIleuIleValIlyrrTrpGluMetGluAspLysAsnIleIleGlnp 67
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209 GCGCACTAATTCCTATTCGGAAATGCGAGATAGAACATTTATTCATTT 258
67 eValIhsglyGluAspleuTyrrValGlnHisSerSerTyrrArpGlna 84
|||||
259 TGTGCATGGAGAGAGACCTGAAAGGTTCCAGCATAGAGCTACACACACA 108
84 rGlaArpLeuLeuLysAspGlnLeuSerLeuGlnAlaIleuGln 100
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309 GGGCCCGCGCTTGAAAGAACACCTCTCCCTGGGAATGCTGCACCTTCAG 358
101 IletThrAspValLysLeuGlnAspAlaGlyValIlyrrArpGlyMetIle 117
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359 ATCACAGATGTGAATTCGAGATGCGAGGGGTGTACCGCTGATGATGAT 408
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ID AAS02120 standard; cDNA: 3575 BP.
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AC AAS02120;
XX 18-JUL-2001 (first entry)
XX Human TANGO 509, alternative CDNA sequence #3.
DE
XX
KW Human: TANGO 499; transmembrane protein; diagnostic; asthma;
KW immunological disorder; arthritis; graft rejection; renal disorder;
KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
KW neurodegenerative disease; Parkinson's disease; SS.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 59..931
FT /tag- a
FT /product- "TANGO 509, alternative transmembrane
protein #3"
XX
XX PN WO200121631-A2.
XX
XX PD 29-MAR-2001.
XX
XX PF 20-SEP-2000; 2000WO-US25982.
XX
XX PR 20-SEP-1999; 99US-0399723.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;
XX
XX DR WPI; 2001-211461/21.
XX
XX DR P-PSDB; AAU01409.
XX
XX PT New nucleic acid encoding INTERCEPT 307, TANGO 511, TANGO 351, TANGO
PT 351, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease -
XX
XX PS Disclosure; Page 348-350; 362pp; English.
XX
XX CC The sequence represents the coding sequence of human TANGO 509,
XX CC alternative transmembrane protein #3. The nucleic acid
XX CC and polypeptide sequences are useful for the diagnosis, prognosis and
XX CC treatment of immunological disorders (e.g. arthritis, graft rejection and
XX CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
XX CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
XX CC related disorders (e.g. cerebral oedema), cerebrovascular diseases
XX CC (ischemia), tumours, prostate-related disorders, pituitary-related
XX CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
XX CC Parkinson's disease).
XX
XX SO Sequence 3575 BP: 1028 A: 717 C: 739 G: 1091 T: 0 other;

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Ratio: 5.200 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.655

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seq_documentation_block:
ID AAS02121 standard: cDNA: 3575 BP.
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XX AC AAS02121:
XX

DE Human TANGO 509, alternative CDNA sequence #2.
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 KW Human: TANGO 499; transmembrane protein; diagnostic; asthma;
 KW immunological disorder; arthritis; graft rejection; renal disorder;
 KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
 KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
 KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
 KW neurodegenerative disease; Parkinson's disease; SS.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 59..931
 FT /*tag= a
 FT /product= "TANGO 509, alternative transmembrane
 FT protein #2"
 FT
 XX
 PN WO200121631-A2.
 XX
 PF 29-MAR-2001.
 XX
 PF 20-SEP-2000; 2000WO-US25982.
 XX
 PR 20-SEP-1999; 99US-0399723.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI KIRST SJ, SHARP JD, FRASER CC, BARNES T, KINGSBURY G;
 XX
 DR WPI; 2001-211461/21.
 DR P-PSDB: AAU01408.
 XX
 PT New nucleic acid encoding INTERCEPT 307, TANGO 511, TANGO 351, TANGO
 PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
 PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
 PT disease.
 XX
 PS Disclosure: Page 345-347; 362pp; English.
 XX
 CC The sequence represents the coding sequence of human TANGO 509,
 CC alternative transmembrane protein #2. The nucleic acid
 CC and polypeptide sequences are useful for the diagnosis, prognosis and
 CC treatment of immunological disorders (e.g. arthritis, graft rejection and
 CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
 CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
 CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.
 CC ischaemia), tumours, prostate-related disorders, pituitary-related
 CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
 CC Parkinson's disease).
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 SQ Sequence 3575 BP; 1029 A; 716 C; 738 G; 1092 T; 0 other:

Alignment_scores:
 Quality: 1507.00 Length: 290
 Ratio: 5.197 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.655

alignment_block:

US-09-649-108-1 x AAS02119

Align seg 1/1 to: AAS02119 from: 1 to: 3575

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109 CGCATTTACTGTCACGCTTCCCAAGACCTATATGTGTGAGGTATGGA 158
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  |||||||
709 GGAAGAACCTATACAGCTGATGTCATGCCACAACTACCTGTGCACATC 758
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284 sPTThrHisLeuGluGluThr 290
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seq_name: /SID52/gcdata/geneseq/geneseq/MN2001.DAT: AAD02772

seq_documentation_block:

ID AAD02772 standard; cDNA; 968 BP.

XX AAD02772;

AC

XX 19-JUN-2001 (first entry)

DT

XX

DE

XX

Human B7-4 secreted (B7-4S) protein cDNA.

KW Human; B7-4 secreted protein; B7-4S; receptor PD-1; chromosome 9; tumour;
KW antiviral; anti-lymphatic; gene mapping; cytostatic; myocardial infarction;
KW atherosclerosis; neurological disease; immunomodulatory; allergy; GVHD;
KW graft-versus-host disease; immunosuppressive disease; organ transplant;
KW acquired immune deficiency syndrome; AIDS; autoimmune disease; therapy;
SS .
XX
XX Homo sapiens.
OS
FH Key
FT CDS
FT
FT sig_peptide
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FT mat_peptide
FT
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XX MO200114557-A1.
XX
PD 01-MAR-2001.
PE 23-AUG-2000; 2000MO-US23347.
XX
PR 23-AUG-1999; 99US-0150390.
PR 10-NOV-1999; 99US-0164897.
XX
PA (DAND) DANA FARBER CANCER INST INC.
PA (GENY) GENETICS INST INC.
XX
PI Wood C, Freeman GJ;
XX WPI: 2001-160116/16.
DR P-PSDB; AAY72676.
DR
XX
PT Treating e.g. cancer or allergies comprises contacting an immune cell
PT with an agent that modulates signalling via PD-1 or B7-4 to modulate the
PT immune response -
XX
XX Example 1; fig 1; 168pp; English.
XX
CC The present CDNA sequence encodes human B7-4 secreted (B7-4S) protein
CC having a short hydrophilic tail without a membrane anchor or a
CC transmembrane domain. The human B7-4 CDNA is isolated from human
CC activated keratinocyte and placental CDNA libraries. B7-4 gene is
CC localised on human chromosome 9.
CC The invention relates to a method for modulating immune response by
CC contacting an immune cell with an agent that modulates signalling via
CC B7-4 or its receptor PD-1. Modulating the interaction between PD-1 and
CC B7-4 modulates a costimulatory or an inhibitory signal in an immune cell,
CC resulting in the modulation of the immune response. The invention is
CC useful for upregulating an immune response to treat tumours, neurological
CC diseases and immunosuppressive diseases or to downregulate an immune
CC response useful in organ transplants, graft-versus-host disease (GVHD),
CC treating allergies and viral infections e.g., acquired immune deficiency
CC syndrome (AIDS). The invention also provides B7-4 or PD-1 fusion proteins
CC which are useful for treating immunological disorders, such as autoimmune
CC diseases e.g., heart disease, myocardial infarction and atherosclerosis
CC or in the case of inhibiting rejection of transplants. These fusion
CC proteins are also used as immunogens to produce anti-B7-4 antibodies.
CC PD-1 is useful in promoting the maintenance of pregnancy. B7-4 protein is
CC highly expressed in placental trophoblasts and plays a role in preventing
CC maternal rejection of the foetus. B7-4 CDNA is also useful for
CC gene mapping.
XX
XX Sequence 968 BP; 314 A; 209 C; 202 G; 243 T; 0 other;

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Quality: 1184.00 Length: 227
Ratio: 5.216 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-649-108-1 x AAD02772 ..

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AC AAD02707;
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DT 31-MAY-2001 (first entry)
XX
DE Human B7-4 secreted (B7-4S) protein cDNA.

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XX Human; B7-4 secreted protein; B7-4S; chromosome 9; antiviral; influenza;
KM immunomodulatory; acquired immune deficiency syndrome; AIDS; anti-tumour;
KM graft-versus-host disease; GVHD; immunological disorder; Herpes disease;
KM autoimmune disease; common cold; shingles disease; encephalitis; therapy;
KM organ transplant; gene mapping; transgenic; viral infection; ss.
OS Homo sapiens.
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XX PD 01-MAR-2001.
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XX P2 23-AUG-2000; 2000MO-US23256.
XX PR 23-AUG-1999; 99US-0150390.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Freeman G, Bousiolis V, Chernova T, Malenkovich N;
XX DR WPI: 2001-202936/20.
XX DR P-SDB: AAY72644.
XX PT New human B7-4 polypeptides useful for enhancing the immune response
XX PT against a viral infection or induce a tumor immunity and to diagnose
XX PT conditions related to aberrant B7-4 expression or activity
XX
XX Claim 1: Fig 1: 123pp: English.
XX
XX CC The present cDNA sequence encodes human B7-4 secreted (B7-4S) protein
XX CC having a short hydrophilic tail without a membrane anchor or a
XX CC transmembrane domain. Human B7-4 protein is isolated from human activated
XX CC keratinocyte and placental cDNA libraries. B7-4 gene is localised on
XX CC human chromosome 9.
XX CC The invention relates to human B7-4 secreted (B7-4S) protein, B7-4
XX CC membrane (B7-4M) protein and their corresponding cDNA molecules. Human
XX CC B7-4 proteins are useful for upregulating immune response to treat viral
XX CC skin diseases such as Herpes disease or shingles disease, systemic viral
XX CC diseases such as Influenza, common cold and encephalitis, and for
XX CC inducing tumour immunity or to downregulate an immune response useful in
XX CC organ transplants, graft-versus-host disease (GVHD), treating allergies
XX CC and viral infections e.g., acquired immune deficiency syndrome (AIDS).
XX CC B7-4 antagonists are used to modulate the T cell co-stimulation by
XX CC contacting an activated T cell with a B7-4 antigen. The invention is also
XX CC used for producing non-human transgenic animals. It also provides B7-4
XX CC fusion proteins which are useful for treating immunological disorders,
XX CC such as autoimmune diseases or in the case of transplantation. B7-4
XX CC fusion proteins are used as immunogens to produce anti-B7-4 antibodies.
XX CC B7-4 cDNA is also useful for gene mapping. Methods are provided
XX CC for modulating the immune response of individuals, by inhibiting or
XX CC enhancing the lymphokine synthesis by the activated T cells. Diagnostic,
XX CC prognostic, pharmacogenetics, screening and therapeutic methods are also
XX CC provided using B7-4 proteins.
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XX SQ Sequence 968 BP; 314 A; 209 C; 202 G; 243 T; 0 other:

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67 eValHisGlyGluGluAspLeuLysValGlnHisSerSerTyrArgGlnA 84
259 TGTGCATGTAGAGAGAGAGACCTGAAGGTTCCACCATATAGTAGTACACACGA 304
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309 GGGCCGGGCTGTTGAAGAGCAGCTCTCCCTGGGAAATGCTGCACATTCAG 358
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359 ATCACAGATGTGAATTCAGAGATGCAGGGGTGTACCCCTCATGATCAG 408
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609 CCAAGAGAGAGAGAGAAAGCTTTTCAATGTGACACACACATGAGAAAC 658
201 ThrThrThrAsnGluIlePheTyrCysThrPheArgGluAspProG 217
659 ACAAAACATTAATGAGATTTTCTACTGCACCTTTAGAGAGATTAAGTCC 708
217 uGlnAsnHisThrAlaGluLeuValIlePro 227
709 GGAAACCATATACAGCTGAATTTGGTTCATCCCA 739

seq_name: /SID52/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH14847
seq_documentation_block:
ID AAH14847 standard; cDNA; 1301 BP.
XX
XX AC AAH14847;
XX
XX DT 26-JUN-2001 (first entry)
XX
XX DE Human cDNA sequence SEQ ID NO:12675.
XX

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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss

XX Homo sapiens.

XX EPI074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

WIPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -

PS Claim 8; SEQ ID 12675; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the amplification

CC of the present invention.

XX

S0 Sequence 1301 BP; 387 A; 261 C; 327 G; 326 T; 0 other:

Alignment_scores:

Quality: 1181.00 Length: 228

Ratio: 5.180 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

US-09-649-108-1 x AAH14847 ..

Align seg 1/1 to: AAH14847 from: 1 to: 1301

63 AsnIleIleGlnPheValHisGlyGluGlnAspLeuLysValGlnHisE 79

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2 AACATTATTCATTTGTCTCATGGAGACAGCACTCGAAGCTCAGCATAG 51

79 rSerTyrrArGgInArgAlaArgLeuLeuLysASpGlnLeuSerLeuGly 96

|||||

52 TAGCTACAGACAGAGGCCCGCTGTGTGAAGACCACTCTCCCTGGAA 101

[illegible]

PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 PI Oka T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 1; SEQ ID 4406; 2537bp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95693 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 CC
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 XX
 alignment_scores:
 Quality: 1177.00 Length: 228
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 Percent Similarity: 100.000 Percent Identity: 99.561
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 63 AaillleleaglPheValHisGlyGluAspLeuLysValGlnHis 79
 2 AACATTATTTCATTTGTCATGAGAGAGAGACCTGAAAGCTTCACATAG 51
 79 rSerTyArgGlnArgAlaArgLeuLeuLysAspGlnLeuSerLeuGly 96
 52 TAGCTACAGACAGAGAGCCGGCTGTGAAGAGACAGCTCTCCGTGGAA 101
 96 snAlaAlaLeuGlnIleThrAspValLysLeuGlnAspAlaGlyValTy 112
 102 ATGCGCGACTTCAGATCAGATGTGAATTCAGAGATGCAAGGCTGTAC 151
 113 ArgCysMetIleSerTyGlyGlyAlaAspTyLysArgGlnIleThrVal 129
 152 CGCTGCATGATCAGCTATGCTGCTCCGACCTACAGCGAATTACTGTGA 201
 129 sValAsnAlaProTyArgLysLysIleAsnGlnArgIleLeuValAsp 146
 202 AGTCATATGCCCATACAAACAAATCAACCAAGATTGTTGCTGATC 251

146 roValThrSerGluHisGlyLeuThrCysGlnAlaGlyTyrProLys 16..
 252 CAGTCACCTCTGACATGAACTGACATGTCAGAGGCTGAGGCCCAAG 301
 163 AlaGluValIleThrPheSerSerAspHisGlnValLeuSerGlyLysTh 179
 302 GCCGAAGTCATCTGGACAGACGTACCACTCAAGTCCTGAGTGGTAAGC 351
 179 rThrThrThrAsnSerLysArgGluGluLysLeuPheAsnValThrSer 196
 352 CACCAACACCAATTCACAGAGAGAGAGAGAGCTTTTCATGACACAGCA 401
 196 hLeuArgGlnLeuAsnThrThrThrAsnGluIlePheTyrCysThrPhe 212
 402 CACTGAGATCAACACACCAACTAATGAGATTCTTCTACTGCACTTTAGG 451
 213 ArgLeuAspProGluGluAsnHisThrAlaGluLeuValIleProGluLe 245
 452 ACATTAGATCTGAGAGAAACCATACAGCTGAATGTCATCTCCAGAAC 501
 229 uProLeuAlaHisProProAsnGluArgThrHisLeuValIleLeuGly 246
 502 ACCTCTGGACATCTCCAAATGAAGAGCTCATTGGTAATTCTGGGAGC 551
 246 laIleLeuLeuCysLeuGlyValAlaLeuThrPheIlePheArgLeuArg 262
 552 CCATCTTTATATGCTTGGTGTACACCTGACATTCATCTTCCTTAAAGA 601
 263 LysGlyArgMetLeuAspValLysCysGlyIleGlnAspThrAsnSe 279
 602 AAGGAGACATATGATGATGTAAGAAATGTGGATCCCAAGATACAAACTC 651
 279 rLysLysGlnSerAspThrHisLeuGluGluThr 290
 652 AAGAAGCAAACTGATACACATTGTCAGAGAGAGC 685
 seq_name: /SIDS2/gcdata/geneseq/geneseqn/M2001.DAT:AAD05068
 seq_documentation_block:
 ID AAD05068 standard; cDNA; 891 BP.
 AC AAD05068;
 XX
 DT 17-JUL-2001 (first entry)
 XX
 DE Human secreted protein-encoding gene 1 cDNA clone HD19P15; SEQ ID NO: 26.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; hematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; B7-H6 protein;
 KW endocrine disorder; infection; wound healing; vulnerability; gene therapy;
 KW cell culture; chemotaxis; food additive; chromosome 9;
 KW binding partner identification; ss.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT 93..830
 FT CDS
 FT /*tag- a
 FT /product= "Human secreted B7-H6 protein"
 FT /transl_except= (pos:420..422, aa:Xaa)
 FT /note= "Xaa is any of the naturally occurring
 FT L-amino acids"
 FT 93..146
 FT sig_peptide
 FT /*tag- b
 FT 147..827
 FT mat_peptide
 FT /*tag- c
 FT /product= "Mature human secreted B7-H6 protein"

FT mat_peptide 67..870
 FT /*tag- c
 PN MO200139722-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US32583.
 XX
 PR 30-NOV-1999; 99US-0451291.
 PR 28-AUG-2000; 2000US-0649108.
 XX
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 XX
 PI Chen L;
 XX
 DR WPI: 2001-397926/42.
 DR P-PSDB: AANU03560.
 XX
 PS Example 7; Fig 10; 85pp: English.

CC The present sequence encoding for novel mouse immunoregulatory protein
 CC B7-H1 (mb7-H1) is capable of co-stimulating T-cells. The sequence for
 CC human B7-H1 (hb7-H1) is also given (AAU03559). B7-H1 is useful for
 CC co-stimulating T-cells such as helper T-cells that provide helper
 CC activity for B-cell antibody-producing response e.g. IgG2a antibody
 CC response, in a mammal having an immunodeficiency disease, inflammatory
 CC condition or an autoimmune disease, by culturing B7-H1 with the
 CC mammalian T-cells in vitro, or administering B7-H1 or a nucleic acid
 CC encoding B7-H1 to the T-cells, such that the level of CD40 ligand on the
 CC T-cell surface is increased. The method further involves providing a
 CC recombinant cell e.g. an antigen presenting cell (APC) which is the
 CC progeny of a cell obtained from the mammal and has been transfected or
 CC transformed ex vivo with a nucleic acid encoding B7-H1, so that the cell
 CC expresses B7-H1, and administering the cell to the mammal. Prior to
 CC administration, the APC is pulsed with an antigen or an antigenic
 CC peptide. B7-H1 can be used to control pathologic cell mediated
 CC conditions (e.g. those induced by infectious agents such as Mycobacterium
 CC tuberculosis) or other pathologic cell mediated responses such as those
 CC involved in autoimmune diseases (e.g. rheumatoid arthritis).
 CC
 XX
 SQ Sequence 873 BP; 243 A; 206 C; 235 G; 189 T; 0 other;

2
 ment_scores:
 Quality: 1050.00 Length: 291
 Ratio: 4.086 Gaps: 2
 Percent Similarity: 88.316 Percent Identity: 69.416

alignment block:
 US-09-649-108-1 x AAS06593

Align seg 1/1 to: AAS06593 from: 1 to: 873

1 MetATGIIlePheAlaValPheIIlePheMetThrTYTTPRHisLeuLeuAs 17
 |||||
 1 ATGAGAGATATTGTCGTCGATATATTCACAGCCTGCTGCACTGCTAGC 50
 17 nAlaPheThrValIThrValProlysAspLeuTYrValValGluTYrGlyS 34
 :|||
 51 GCGCTTACTATACGCGCTCCAAAGAGACTTGAACGTCGTGAGATGGCA 100
 34 eTAspMetThrIleGlyCysLysPheProValGluLysIleLeuAspLeu 50
 |||||
 101 GCAACGTACGATGGAGTGCAGATTCCCTGTAGAACGGAGCTGGACCTG 150
 51 AlaAlaLeuIleValTYrTPRHisMetGluAspLysAsnIleIleGlnP 67
 |||||
 151 CTGCGCTTAGCTGCTACTGGGAAAGAGATGAGCAAGTATTCAGTT 200

67 eValHisGlyGluGluAspLeuLysValGlnHisSerSerTYrArgGln 84
 |||||
 201 TGTGGCAGAGAGAGAGACCTTAAGCCTTCAGACAGCAACCTTCACGGGCA 250
 84 rGAlaArgLeuLeuLysAspGlnLeuSerLeuGlyAsnAlaAlaLeuGln 100
 |||||
 251 GAGCCTCGCTGCCAAAGACCAGCTTTGCAAGGGAATTCCTCCCTTCAG 300
 101 IleThrAspValLysLeuGlnAspAlaGlyValTYrArgCysMetIleSe 117
 |||||
 301 ATCACAGACGTCAAGCTGCAGAGCCGCTTACTGCTGCATATACG 350
 117 rTYrGlyGlyAlaAspTYrLysArgIlePheValLysValAsnAlaProT 134
 |||||
 351 CTACGGTGTGCGGACTACCAAGCAATCACGCTGAAGATCATATGCCCAT 401
 134 yTAsnLysIleAsnGlnArgIleLeuValValAspProValThrSerGlu 150
 |||||
 401 ACCGCAAAATCAACACAGAAAT...TCGCTGATCCAGCCACTTCAG 450
 151 HisGluLeuThrCysGlnAlaGluTYrProLysAlaGlnValIleP 167
 |||||
 448 CATGAACCTAATATGTCAGGCCGAGGCTTATCCAGAACTGAGCTAATCTG 497
 167 PHisSerSerAspHisGlnValLeuSerGlyLysThrThrThrAsnS 184
 |||||
 498 GACAAACAGTGCACCAACCCGCTAGTGGAGAAAGATGTCACACACTT 547
 184 eTyrArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 201
 |||||
 548 CCCGACAGAGGGGATGCTTCAATGTGACCAAGCATCTGAGGCTCAAC 597
 201 ThrThrThrAsnGluIlePheTYrCysThrPheArgArgLeuAspProG 217
 |||||
 598 GGCACAGCGAATGATGTTTCTACGTACGTTTGGAGATCCACACCAAG 647
 217 uGluAsnHisThrAlaGluLeuValIleProGluLeuProLeuAlaHis 234
 |||||
 648 GCMAAACCCACACAGCGGAGCTGATCATCCAGAACTGCTGCACACATC 700
 234 rPRAsnGluArgThrHisLeuValIleLeuGlyAlaIleLeuLeuCys 250
 |||||
 698 CTCACAGACAGAGACTACGTCGTCCTTCGATCCATCTCTGTTC 747
 251 LeuGlyValAlaLeuThrPheIlePheArgLeuArgGlyGly...ArgHis 266
 |||||
 748 CTCATTGTAGTGTCCACGCTCCTCTCTTGTGAGAAAAACAAGTGAAGAT 797
 266 tMetAspValLysLysCysGlyIleGlnAspThrAsnSerLysLysGln 283
 |||||
 798 GCTAGATGCGAGAAATGTGGCTTGAAGATACAAAGCTCAAAAACCGAA 847
 283 eTAspThrHisLeuGluGluTYr 290
 |||||
 848 ATGATACACAATTCAGAGAGACG 870


```

;
; AUTHORS: FREEMAN, GORDON J.
; AUTHORS: FREEDMAN, ARNOLD S.
; AUTHORS: SEGIL, JEFFREY M.
; AUTHORS: LEE, GRACE
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
; TITLE: B7, A New Member Of The Ig Superfamily With
; TITLE: Unique Expression On Activated And Neoplastic B Cells
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1491
; US-08-147-772-1

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Quality: 176.50      Length: 279
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US-09-649-108-1 x US-08-147-772-1 ..
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444  AAGAAGAGGCAACCGCTGCTGCTGATGATGCTGGGACATGTAATTA 488
41  SPheProValaGluYrGluLeuAspLeuAlaLeuIleValaYrTrpG 58
    .....GACCTGGCACAACTGCGACATCTACTGCG 516
489  LmetsLusPlysaSnIleIleGlnPheValHisGlyGluLusPleu 74
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517  AAAGGAGAGAAATGCTGCTGATGATGCTGGGACATGTAATTA 566
75  LysValaGlnHisSerSerYrArgGlnArgAlaArgLeuLeuLysAsp 91
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567  TGGCCGAGTACAAAGAC.....CGACCATCTTGCAT.. 599
91  nLeuSerLeuGlnAsnAlaLeuGlnIleThrAspValLysLeuGlna 108
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600  ...ATCACTAATAACCTCTCATGTGTCTGCTGCTGCTGCTGCTG 645
108  SPAlaGlyValaYrArgCysMetIle...SerYrGlyGlyAlaAspYr 123
    |||:|||||:|||||:|||||:|||||:|||||:
646  ACGAGGCGACATACGAGTGTGTCTGTAAGTATGAAAGACCTTTC 695
124  LysArg.....IleThrValLysValAsnAlaPr 133
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133  cYrAsnLysIleAsnGlnArgIleLeuValaLysProValaIleThrSer 150
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746  TACACCTAGTATATCTGACTTGAAT.....CCAACTTCTAATA 786
150  LuHisGlnLeuThrCysGlnAlaGlu...GlyTrpProLysAlaGluVal 165
    :|||:|||||:|||||:|||||:|||||:|||||:
787  TTAGAAGGATATTTGCTCAACCTCTGAGAGGTTTCCAGAGCTCACTC 836
166  IleTrpTrpSerSerAspHisGlnValaLeuSerGlyLysTrpThrTh 182
    |||:|||||:|||||:|||||:|||||:|||||:
837  TCCGTGTTGGAATGGAAGAA...TTAAATGCCATCAACACAAAGT 883
182  rAsnSerLysArgGluGluLysLeuPheAsnValaThrSerThrLeuArg 199
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884  TTCCCAAGATCTGTAAGTCTATATGCTGTAGACAGCAAACTGAT 933
199  leAsnThrThrAsnGlnIlePheYrCys..... 209
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934  TCAATATGACAAACCAACACCTTCATGTCTTCATCACTATGACAT 984
210  .....ThrPheArgArgLeuAspProGluGluAsnHisTh 241
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984  TTAAGATGATACAGACCTTCACATGGAATACAAACCAAGCAAGT 1033
221  rAlaGluLeuValaIleProGluLeuProLeuAlaHisProPheAsn 238
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1034  TCCGTATACCTGCTCCATCTGCGGCAT..... 1064
238  rGThrHisLeuValaIleLeuGlyAlaIleLeuLeuCysLeuGlyVala 254
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1065  ..ACCTATATCTCACTAATGAAATTTTGTGATATGC.....TGC 1103
255  LeuThrPheIlePhe.....Ar 260
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1104  CTGACCTACTGCTTTGCCCCAAGATGACAGAGAGAAAGAGAGATGAG 1154
260  gLeuArgLysGlyArgMetLysPvalLysLysCys 272
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seq_name: /cgn2_6/prodata/2/lna/5b_comb.seq:US-08-456-104-5
seq_documentation_block:
; Sequence 5, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; TISSUE TYPE: lymphoid
; CELL TYPE: B cell
; CELL LINE: Raj1

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1 PUBLICATION INFORMATION:
2 AUTHORS: FREEMAN, GORDON J.
3 AUTHORS: FREEDMAN, ARNOLD S.
4 AUTHORS: SEGIL, JEFFREY M.
5 AUTHORS: LEE, GRACE
6 AUTHORS: WHITMAN, JAMES F.
7 AUTHORS: NADLER, LEE M.
8 TITLE: 87, A New Member Of The Ig Superfamily With
9 TITLE: Unique Expression On Activated And Neoplastic B Cells
10 JOURNAL: The Journal of Immunology
11 VOLUME: 143
12 ISSUE: 8
13 PAGES: 2714-2722
14 DATE: 15-OCT-1989
15 RELEVANT RESIDUES IN SEQ ID NO: 22: FROM 1 TO 1491
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17 US-08-101-624-22
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seq_name: /cgn2_6/ptdata/2/1na/5B_COMP.seq:US-08-751-767A-5

seq_documentation_block:
/ Sequence 5, Application US/08751767A
/ Patent No. 5994104
/ GENERAL INFORMATION:
/ APPLICANT: ANDERSON, ROBERT J.
/ APPLICANT: GRANT, HUGH
/ APPLICANT: MACDONALD, IAN D.
/ TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
/ NUMBER OF SEQUENCES: 80
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: NIXON & VANDERHIVE P. C.
/ STREET: 1100 NORTH GLEBE ROAD
/ CITY: ARLINGTON
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22201
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/751,767A
/ FILING DATE: 08-NOV-1996
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: SADOFF, B. J.
/ REGISTRATION NUMBER: 36,663
/ REFERENCE/DOCKET NUMBER: 117-221
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 70381641091
/ TELEFAX: 7038164100
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1491 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 318..1181
/ US-08-751-767A-5

alignment_scores:
Quality: 176.50 Length: 279
Ratio: 1.177 Gaps: 12

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APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raj1
IMMEDIATE SOURCE:
LIBRARY: cDNA in pCDM8 vector
CLONE: B7, Raj1 clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
FEATURE:
NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
FEATURE:
NAME/KEY: Alternate polyadenylation signal
LOCATION: 1474 to 1479 bp
IDENTIFICATION METHOD: similarity to other pattern
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: MADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 28: FROM 1 TO 1491
US-08-280-757B-28

alignment_scores:
Quality: 176.50 Length: 279
Ratio: 1.177 Gaps: 12
Percent Similarity: 53.763 Percent Identity: 21.505

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91 nLeuSerLeuGlnAlaIleuGlnIleThrasPValLysLeuGln 108
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seq_documentation_block:
; Sequence 1, Application US/09159135
; Patent No. 6149905
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raji
IMMEDIATE SOURCE:
LIBRARY: cDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3

FEATURE:
NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern

FEATURE:
NAME/KEY: Alternate polyadenylation signal
LOCATION: 1474 to 1479 bp
IDENTIFICATION METHOD: similarity to other pattern

PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989

RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1491

US-09-159-135-1

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alignment_scores:
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    Ratio: 1.177
    Length: 279
    Gaps: 12
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Percent Similarity: 53.763 Percent Identity: 21.505
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alignment_block: uc-00-640-100-1 uc-00-150-125-1
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Align seg 1/1 to: US-09-159-135-1 from: 1 to: 1491

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seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-08-205-697A-18
seq_documentation_block:
; Sequence 18, Application US/08205697A
; Patent No. 6218510
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor,
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO. 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 318..1181
US-08-205-697A-18
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Quality: 176.50 Length: 279
Ratio: 1.177 Gaps: 12
Percent Similarity: 53.763 Percent Identity: 21.505
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489 .....GAGCTGGCAACAACTCCGATCTACTGCG 516
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255 LeuThrPheIlePhe.....Ar 260
1104 CTGACCTACTGCTTTGCCCCCAAGTTCGACAGACAGAAAGAGATGAGAG 1153
260 gLeuArgLysGlyArgMetLeuAlaValLysLysCys 272
1154 ATTGAGAAAGGAAAGTGTACGCCCTGTATTAACAGTGT 1190

seq_name: /cogn2_6/prodata/2/lna/5b_COMB.seq:US-08-702-525-18

seq_documentation_block:
: Sequence 18, Application US/08702525
: Patent No. 6294660
: GENERAL INFORMATION:
: APPLICANT: Sharpe, Sharpe
: APPLICANT: Borjello, Francescopolo
: APPLICANT: Freeman, Gordon
: APPLICANT: Nadler, Lee
: TITLE OF INVENTION: NO. 6294660el Forms of T Cell Costimulatory
: MOLECULES AND USES THEREFOR
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHYTE & COCKFIELD
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts

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117 ..... ||| ..... |||
127 AAGAAGTGGCAACGCTGCTGTCGACAAATGTTCTTGAA..... 171
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58 lunetgluasplysasnillelelphelphelhisglugluaspheu 74
200 AAAGAGAGAAAGAAATGGTCTGACTATGATGCTGGGACATGAAATA 249
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250 TGGCCCGAGTACAAAGAAC.....CGAGCATCTTTGAT.. 282
91 nleuserleuglyasnalaaleuulinlethraspvallysleuglna 108
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124 lysarg.....lethrvallysvalasnalaapr 133
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166 lletprthserasphhisglinvalleuserglylysthrthtrth 182
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seq_name: /cgn2_6/plodata/2/lna/5B_COMB.seq:US-08-458-356-207

seq_documentation_block:

; Sequence 207, Application US/08458356

; Patent No. 5942235

; GENERAL INFORMATION:

; APPLICANT: Proietti, Enzo

; APPLICANT: Tartaglia, James

; APPLICANT: Cox, William I.

; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY

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? NUMBER OF SEQUENCES: 217
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Curtis Morris & Salford
? STREET: 530 Fifth Avenue
? CITY: New York
? STATE: NY
? COUNTRY: USA
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/458,356
? FILING DATE: 02-JUN-1995
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/184,009
? FILING DATE: 19-JAN-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Frommer, William S.
? REGISTRATION NUMBER: 25,506
? REFERENCE/DOCKET NUMBER: 454310-2530
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 840-3333
? TELEFAX: (212) 840-0712
? TELEX: 42506CORTMS
? INFORMATION FOR SEQ ID NO: 207:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 867 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? US-08-458-356-207

alignment_scores:
Quality: 172.00 Length: 263
Ratio: 1.178 Gaps: 12
Percent Similarity: 55.513 Percent Identity: 22.053

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41 sphenovalglulysglinleuaspheulaalaleuilevaltytrpg 58
172 ..... ||| ..... |||
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200 AAAGAGAGAAAGAAATGGTCTGACTATGATGCTGGGACATGAAATA 249
75 lysvalglinhissersertyrarglnargalargleuleuylsaspj 91
250 TGGCCCGAGTACAAAGAAC.....CGAGCATCTTTGAT.. 282
91 nleuserleuglyasnalaaleuulinlethraspvallysleuglna 108
283 ....ATCACTAATTAACCTCTCCATTGTGATCTGGCTCGGCCCATCTG 328
108 spaliaglyvaltyrargysmetile...sertyrglyglialaasptyr 123
329 ACAGAGGCACATACGAGTGTGTCTTCTGAAGTATCAAAAAGACGCTTC 378
124 lysarg.....lethrvallysvalasnalaapr 133

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379 AAGCGGACACCCTGGCTGCAGTGAAGCATTAATGACCAAGCAGTCGACTGCC 428
133 ctyrgrnlyslleagnglnarglleuleuValysprovalthrserg 150
429 TACACCTAATAATGTGACTTTGAATT.....CCAACTTTAATA 469
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470 TTAGAAGGATTAATTTCCTAACCTTGAGAGGTTCCTCACAGGCTCACCCTC 519
166 lletprrhserseraphisiclnalleuserglylsthThThTh 182
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667 TTAAAGATGAATCAGACTTCAACGTGAATACACCAAGCAGACACTTT 716
221 rAlagluenuValleProgluleuProleuAlahIsProproAsnguIua 238
717 TCCTGTATACCTGCTGCCACTCTCTGGGCCATT..... 747
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255 leuthrPhelIeph.....ArgleuarqLysglYatg 265
787 CTGACCTACTGCTTTGGCCCCCAAGATTCAGAGAGAGAGAG 825

seq_name: /cgn2_6/prodata/2/lma/6B_COMB.seq-US-08-812-946A-2

seq_documentation_block:
Sequence 2, Application US/08812946A
Patent No. 6221637
GENERAL INFORMATION:
APPLICANT: Tsuneaki HIDA et al.
TITLE OF INVENTION: XANTHENE DERIVATIVES, THEIR PRODUCTION AND
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,946A
FILING DATE: March 4, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

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      TELEPHONE: 202-971-8850
      TELEFAX:
      TELEX:
      INFORMATION FOR SEQ ID NO: 2:
      SEQUENCE CHARACTERISTICS:
          LENGTH: 867 bases
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      US-08-812-946A-2

alignment_scores:
    Quality: 172.00      Length: 263
    Ratio: 1.178        Gaps: 12
    Percent Similarity: 55.513   Percent Identity: 22.053

alignment_block:
US-09-649-108-1 x US-08-812-946A-2 ..

Align seg 1/1 to: US-08-812-946A-2 from: 1 to: 867

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:: ||| ||| : : : : : ||| : : : : :
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250 TGGCCGCACTACAAAC.....
91 nleuSerleugLyasnAlalaLeuGlnIleThrasPvallysLeuSluA 108
||||| : : : : : |||
283 ... ATCACTAATAAACCTTCCATTGTGATCTGCTGCCGCCACATCTG 378
108 spralagLYvalTYrArgySmelle..serTYrgLYglYAlaAsprTYr 124
|| | ||| : : : : : ||| : : : : :
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124 LysArG.....IleThrValLysValAsnAlar 133
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